

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model  
Run on: July 18, 2003, 19:01:57 ; Search time 4798 Seconds  
(without alignments)  
11239.579 Million cell updates/sec  
Title: US-09-977-221-2-C-AT-1513  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 2054640 seqs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
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5: gb\_ov:\*  
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8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
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12: gb\_sy:\*  
13: gb\_un:\*  
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38: en\_sy:\*  
39: en\_hgt\_hum:\*  
40: en\_hgt\_mus:\*  
41: en\_hgt\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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4	1836.6	99.1	2164	9	BC011913	BC011913 Homo sapi
5	1835	99.0	2168	6	AX099420	AX099420 Sequence
6	1428	77.1	2011	9	AK090866	AK090866 Homo sapi
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ALIGNMENTS

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DEFINITION Sequence 2 from Patent EP1199372.  
ACCESSION AX427649  
VERSION AX427649.1 GI:21537769  
KEYWORDS human.  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Morten J.E.  
TITLE Polymorphisms in the human p2x7 gene  
JOURNAL Patent: EP 1199372-A 2 24-APR-2002;











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DEFINITION			
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ACCESSION			
AX099420			
VERSION			
AX099420.1			
GI:13538536			
KEYWORDS			
human.			
SOURCE			
human.			
ORGANISM			
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
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JACOBS,K., MCCOY,J.M., LAVALLIE,E.R., COLLINS-RACIE,L.A., EVANS,C.,			
MERBERG,D., TREACY,M., BOWMAN,M.R., SPAULDING,V. and AGOSTINO,M.J.			
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Patent: WO 0119988-A 60 22-MAR-2001;			
Genetics Institute, Inc. (US)			
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ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
  
REFERENCE  
1 Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai, H., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Negatani, K., Masuhara, Y., Negai, K. and Isogai, T.  
NEDO human cDNA sequencing project  
Unpublished  
2 (bases 1 to 2011)  
Isogai, T. and Yamamoto, J.  
Direct Submission  
JOURNAL  
Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazuo-kamatari, Kisarazu, Chiba 252-0812, Japan  
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)  
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.  
  
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SOURCE     house mouse.
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            Simon, J.
            Direct Submission
            Submitted (28-JUL-1998) Simon J., Department of Pharmacology,
            University of Cambridge, Glaxo Institute of Applied Pharmacology,
            Tennis Court Road, Cambridge, CB2 1QJ, UNITED KINGDOM
            2 (bases 1 to 1810)
            Chessel, I.P.; Simon, J.; Hibell, A.D.; Michel, A.D.; Barnard, E.A. and
            Humphrey, P.P.A.
            Cloning and functional characterisation of the mouse P2X7 receptor
            FEBS Lett. 4390, 260-300 (1998)
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Db 552 CTCCTGAGAGCGCGCAAAACCTTCACTGTCTATCAAGACAATATGACTTCCCGGC 611
QY 627 CACAACCTACACGAGCAACATCTCTGCGAGTTTAAACATCACTTGTACTTCCCAAG 686
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Db 6000 TT 6001

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SEQUENCE, 7 unordered pieces.  
AC069209  
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HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP; HTGS\_ACTIVEFIN.  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 228935)  
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,  
Alsbrooks,S.L., Amarantunge,H.C., Are,J.R., Ayele,M., Banks,P.,  
Barbata,J., Benton,J., Bimaye,K., Blankenburg,K., Bonin,D.,  
Bouck,J., Bowie,S., Brivela,M., Brown,E., Brown,M., Bryant,N.P.,  
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Scherer,S., Scott,G., Shen,H., Shoohartari,N., Sisson,I.,  
Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H.,  
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,  
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Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,  
Williams,G., Williamson,A., Wlezyk,R., Wooden,S., Worley,K.,  
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,  
Weinstock,G. and Gibbs,R.  
Direct Submission  
Unpublished  
2 (bases 1 to 228935)  
Worley,K.C.  
Direct Submission  
Submitted (22-MAY-2000) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 228935)  
Worley,K.C.  
Direct Submission  
Submitted (31-JUL-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
On Jul 25, 2002 this sequence version replaced gi:21908286.  
----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: http://www.hgsc.bcm.tmc.edu/  
Drafting Center Code: BCM  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: HATC  
Center clone name: RP11-340F14  
----- Summary Statistics  
Sequencing vector: Plasmid;  
Sequencing vector: M13;  
Chemistry: Dye-terminator Big Dye; 18% of reads  
Assembly program: Phrap; version 0.990329  
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Consensus quality: 228951 bases at least Q30  
Consensus quality: 229319 bases at least Q20  
Estimated insert size: 217327; sum-of-contigs estimation  
Quality coverage: 11x in Q20 bases; sum-of-contigs estimation  
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\* NOTE: Estimated insert size may differ from sequence length  
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.html).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 7 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\* 1 2131: contig of 2131 bp in length  
\* 2132: gap of unknown length  
\* 2232 4621: contig of 2390 bp in length  
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\* 4622 11439: contig of 6718 bp in length  
\* 11440 11539: gap of unknown length  
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\* 20933 21032: gap of unknown length

\* 21033 29597: contig of 8565 bp in length  
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DEFINITION Bos taurus P2X7 mRNA, partial cds.  
ACCESSION AF083073  
VERSION AF083073.1 GI:5880352  
KEYWORDS  
SOURCE Bos taurus.  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.  
REFERENCE 1 (bases 1 to 504)  
AUTHORS Smith, R.A. and Estes, D.M.

TITLE Direct Submission  
JOURNAL Submitted (07-AUG-1998) Veterinary Pathobiology, University of Missouri, 201 Conaway Hall, Columbia, MO 65211, USA  
FEATURES  
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BASE COUNT 138 a 106 c 138 g 122 t  
ORIGIN  
Query Match 21.1%; Score 390.2; DB 4; Length 504;  
Best Local Similarity 85.7%; Pred. No. 5e-89;  
Matches 431; Conservative 2; Mismatches 70; Indels 0; Gaps 0;  
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QY 87 ATCCAGAGATGAATTAATGACCAATTAAGTGTCTTCCACGTGATCATCTTTCTTAC 146  
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RESULT 14  
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56 unordered pieces.  
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VERSION AC130133.1 GI:22138361  
KEYWORDS HTG; HTGS\_PHASE1.  
SOURCE Norway rat.  
ORGANISM Rattus norvegicus  
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE  
AUTHORS

Rattus.  
1 (bases 1 to 115282)  
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,  
Alsbrooks,S.L., Amarantunge,H.C., Are,J.R., Avele,M., Banks,T.,  
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Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,  
Weinstock,G. and Gibbs,R.  
Direct Submission  
Unpublished  
2 (bases 1 to 115282)  
Worley,K.C.  
Direct Submission  
Submitted (08-AUG-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: GHVX  
Center clone name: CH230-83K8  
----- Summary Statistics  
Sequencing vector: Plasmid;  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 56769 bases at least Q40  
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Consensus quality: 61794 bases at least Q20  
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\* NOTE: Estimated insert size may differ from sequence length  
\* (see <http://www.hgsc.bcm.tmc.edu/docs/Genbankdraft.data.html>).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 56 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

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* 97042 97141: gap of unknown length
* 97142 99551: contig of 2810 bp in length
* 99552 100511: gap of unknown length
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* 107841 107941: gap of unknown length
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QY 1792 GTGGCTTCAAGAGTCTTACTGA 1814
DB 104925 GTGGCTTCAAGATCCCTACTGA 104903

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DEFINITION Mus musculus clone RP23-37P22, LOW-PASS SEQUENCE SAMPLING.
ACCESSION AC117579
VERSION AC117579.2 GI:20976671
KEYWORDS HTG; HTGS_PHASE0.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 66872)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Mus musculus, clone RP23-37P22
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 66872)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Bouckgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collamore,A.,
Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
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Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (10-APR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE 3 (bases 1 to 66872)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L.,
Bouckgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
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Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S.,
Schupack,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N.,

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Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S.,  
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Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,  
Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

# TITLE JOURNAL

Submitted (18-MAY-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On May 18, 2002 this sequence version replaced gi:20128322.

## COMMENT

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997).  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: [sequence.submissions@genome.wi.mit.edu](mailto:sequence.submissions@genome.wi.mit.edu)

----- Project Information

Center project name: L23320

Center clone name: 37\_P\_22

\*\*\* NOTE: This record contains 85 individual  
\*\*\* sequencing reads that have not been assembled into  
\*\*\* contigs. Runs of N are used to separate the reads  
\*\*\* and the order in which they appear is completely  
\*\*\* arbitrary. Low-pass sequence sampling is useful for  
\*\*\* identifying clones that may be gene-rich and allows  
\*\*\* overlap relationships among clones to be deduced.  
\*\*\* However, it should not be assumed that this clone  
\*\*\* will be sequenced to completion. In the event that  
\*\*\* the record is updated, the accession number will  
\*\*\* be preserved.

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Job time : 4809 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 18, 2003, 19:00:18 ; Search time 446 Seconds

(without alignments)  
9356.397 Million cell updates/sec

Title: US-09-977-221-2-C-AT-1513

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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	1845.4	99.6	1853	24	AA43027	Human P2X7 gene co
2	1843.8	99.5	1853	22	AAC63694	Human P2X7/p22 co
3	1835	99.0	2168	22	AAF98411	Human cDNA clone C
4	1832.2	98.9	2169	19	AAV30932	Human secreted pro
5	1281.2	69.1	3540	22	AAC63693	Rat P2X7/p22 codi
6	237	12.8	1762	19	AAV27197	HPUR nucleic acid
7	235.4	12.7	1206	22	AAH25211	Nucleotide sequenc
8	235.4	12.7	1759	18	AAV09307	Human brain P2X-1
9	234.6	12.7	1997	17	AAT33853	Rat superior cervi

10	233.8	12.6	1207	22	AA404979	Human purinergic r
11	227.2	12.3	1807	18	AAV09308	Human brain P2X-2
12	203.8	11.0	2633	24	ABK84338	Human cDNA differe
13	203.8	11.0	2633	24	ABL70017	Pancreas cancer re
14	203.8	11.0	2643	17	AAT33855	Human urinary blad
15	196.4	10.6	294	20	AAV89619	EST clone CO390.
16	168.8	9.1	1784	23	AAV76004	DNA encoding novel
17	159.6	8.6	1837	17	AAT33852	Rat vas deferens P
18	148.4	8.0	1272	20	AAV87357	Human P2X3 puriner
19	148.4	8.0	1272	21	AAC64099	Human P2X-3 recept
20	148.4	8.0	1272	22	AA404964	Human P2X3 cDNA 5'
21	148	8.0	1243	20	AAV87356	Human P2X3 puriner
22	148	8.0	1243	21	AAC64101	Human P2X-3 recept
23	148	8.0	1243	22	AA404966	Human purinergic r
24	147.4	8.0	4900	24	AA43026	Human P2X7 gene 5'
25	145.8	7.9	1272	22	AA404988	Human P2X3 cDNA 5'
26	142.6	7.7	11266	24	AA43028	Human P2X7 gene in
27	140.2	7.6	1753	17	AAT33854	Rat dorsal root ga
28	140	7.6	1421	21	AAZ51322	Human purino recep
29	140	7.6	1421	22	AAH25208	Nucleotide sequenc
30	140	7.6	1436	21	AAZ51321	Human purino recep
31	140	7.6	1436	22	AAH25207	Nucleotide sequenc
32	138.6	7.5	1240	22	AA404982	Human purinergic r
33	138.4	7.5	1349	21	AAZ51323	Human purino recep
34	138.4	7.5	1349	22	AAH25209	Nucleotide sequenc
35	138.2	7.5	1639	23	ABK43717	DNA encoding novel
36	135.6	7.3	1499	21	AAZ51324	Human purino recep
37	135.6	7.3	1499	22	AAH25210	Nucleotide sequenc
38	111.6	6.0	564	22	AAI92047	Human polynucleoti
39	111	6.0	1697	19	AAV61833	Coding sequence fo
40	109.4	5.9	1293	19	AAV61832	Coding sequence fo
41	107.8	5.8	1360	22	AA404978	Human purinergic r
42	102.6	5.5	1956	24	ABK09794	Human ovarian tumo
43	102.6	5.5	1986	24	ABK84358	Human cDNA differe
44	101.2	5.5	1973	24	ABN59853	Novel human coding
45	96.8	5.2	878	15	AAQ73761	RP-2 Programmed ce

#### ALIGNMENTS

RESULT 1	
AA43027	
ID	AA43027 standard; DNA: 1853 BP.
XX	
AC	AA43027;
XX	
DT	08-AUG-2002 (first entry)
XX	
DE	Human P2X7 gene coding sequence.
XX	
KW	Human; ds; single nucleotide polymorphism; SNP; P2X7-associated disorder;
KW	inflammation; immune disease; drug development; genetic marker; gene;
KW	P2X7 gene.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	27..1814
FT	/*tag= a
FT	/product= "Human P2X7 protein"
FT	replace (253, C)
FT	/*tag= b
FT	/note= "Single nucleotide polymorphism"
FT	replace (488, A)
FT	/*tag= c
FT	/note= "Single nucleotide polymorphism"
FT	replace (489, T)
FT	/*tag= d
FT	/note= "Single nucleotide polymorphism"
FT	replace (760, G)
FT	/*tag= e
FT	/note= "Single nucleotide polymorphism"





QY	481	GTGTA	CTR	RYAT	GAAGG	AAACAG	AGAC	CTGT	GAAG	CTCT	CTG	CCCT	GGT	GCC	CCCAT	CGAGG	540						
Db	481																540						
QY	541	CAGT	GG	AA	GAGG	CCCCCG	CGCT	CTCT	CTT	GA	CA	AGT	GGCG	AAAA	CACT	TC	AGT	GT	GC	TCA	600		
Db	541																			600			
QY	601	TCA	AG	AA	CA	AT	TC	GACT	TC	CCCG	GC	CA	CA	CT	TAC	CA	CC	AG	AA	CA	CT	660	
Db	601																				660		
QY	661	TAA	CA	CA	CT	CT	TG	AC	CT	TG	CA	AG	AC	TCA	GA	AT	CC	AG	TC	GT	CC	720	
Db	661																				720		
QY	721	GAG	CA	CT	CT	TC	CG	AA	AA	CAG	CG	CA	TAA	TTT	TC	AG	AT	TC	AG	GG	CG	780	
Db	721																				780		
QY	781	TGG	GC	AT	GA	CT	GA	CT	TC	GG	AG	CT	GC	AA	CT	AG	AC	CG	TT	GG	TC	840	
Db	781																				840		
QY	841	AAT	AC	AG	TT	TC	CG	CT	TT	GA	CA	CA	AG	CA	CA	CG	TT	CG	TC	TT	GG	900	
Db	841																				900		
QY	901	ACT	T	CAG	AT	CA	CG	CA	AG	CT	AC	AA	CA	AA	CT	TT	G	A	AA	CG	CA	CT	960
Db	901																				960		
QY	961	TC	TT	CG	GA	CT	CG	TT	T	G	A	CA	T	CT	GG	T	T	G	G	A	CA	T	1020
Db	961																				1020		
QY	1021	AG	CT	GG	TT	GT	GA	CT	CG	CT	CA	AC	CT	CT	CT	CT	CT	CT	CT	CT	CT	1080	
Db	1021																				1080		
QY	1081	ACT	T	CC	TA	CT	AG	CA	ST	T	ACT	CC	AG	T	GC	T	CG	CT	CC	CA	T	1140	
Db	1081																				1140		
QY	1141	AG	T	CT	CT	CA	CC	CT	GT	GT	CA	CA	AT	CT	CT	CA	AG	GA	AG	T	CC	1200	
Db	1141																				1200		
QY	1201	TG	GA	CC	AA	AG	CG	CA	T	T	AA	GT	AT	GT	CT	TT	T	G	AT	GC	CA	1260	
Db	1201																				1260		
QY	1261	TGA	ACC	AG	CA	GT	T	ACT	AG	AG	T	CT	GA	AG	T	CT	CA	AG	GG	CG	CA	1320	
Db																							

QY	1561	TGTTTCAGAAAGCTGGCTTCCTTCCTCCAGACACAGTCTCTGCAGTTCTCTCTCTACCAAGAGC	1620		
DB	1561	TGTTTCAGAAAGCTGGCTTCCTTCCTCCAGACACAGTCTCTGCAGTTCTCTCTCTACCAAGAGC	1620		
QY	1621	CGTTGCTKGGCGCTGGATGTGGATTCCACCAACAGCGGCTGGCGACTGTGCGCTACAGGT	1680		
DB	1621	CGTTGCTGGCGCTGGATGTGGATTCCACCAACAGCGGCTGGCGACTGTGCGCTACAGGT	1680		
QY	1681	GCTACGCCCACTGGCGCTTCGGCTCCCGAGCAGCATGGCTGACTTTGCCATCTGCGCCAGCT	1740		
DB	1681	GCTACGCCCACTGGCGCTTCGGCTCCCGAGCAGCATGGCTGACTTTGCCATCTGCGCCAGCT	1740		
QY	1741	GCTGCGCGCTGGAGATCCGGAAAGAGTTTCCRAAGAGTGAAGGCGAGTACAGTGGCTTCA	1800		
DB	1741	GCTGCGCGCTGGAGATCCGGAAAGAGTTTCCRAAGAGTGAAGGCGAGTACAGTGGCTTCA	1800		
QY	1801	AGAGTCCTTACTGAAGCCAGGACCGTGGCTCAGCTGTGTAATCCCACTTTT	1853		
DB	1801	AGAGTCCTTACTGAAGCCAGGACCGTGGCTCAGCTGTGTAATCCCACTTTT	1853		
RESULT 3					
AAF98411					
ID	AAF98411 standard; cDNA; 2168 BP.				
XX	AC	AAF98411;			
XX	AC	AAF98411;			
DT	07-JUN-2001 (first entry)				
XX	Human cDNA clone C0390_1 sequence SEQ ID 60.				
DE	Human; secreted protein; nutrient; cytokine modulator; proliferation;				
KW	differentiation; immune system modulator; tissue growth; chemotactic;				
KW	haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ss;				
KW	haematopoiesis.				
XX					
OS	Homo sapiens.				
XX					
PN	W0200119988-AL.				
XX					
PD	22-MAR-2001.				
XX					
PF	14-SEP-2000; 2000WO-US25135.				
XX					
PR	17-SEP-1999; 99US-0398829.				
XX					
PA	(GEMY ) GENETICS INST INC.				
XX					
PI	Jacobs K, McCoy JM, LaVallie ER, Collins-Racie LA, Evans C;				
PI	Merberg D, Treacy M, Bowman MR, Spaulding V, Agostino MJ;				
XX					
DR	WPI; 2001-244801/25.				
DR	P-PSDB; AAB90689.				
XX					
PT	Isolated nucleic acids encoding polypeptides, useful for modulating				
PT	e.g. cytokine and cell proliferation/differentiation activity, the				
PT	immune system and hematopoiesis regulating activity -				
XX					
PS	Disclosure; Page 419; 557pp; English.				
XX					
CC	Human cDNA clones represented in AAF98374 - AAF98489 encode secreted				
CC	proteins AAB90667 - AAB90750. The cDNA clones are isolated from various				
CC	tissue types, and may be used in the prevention, treatment and diagnosis				
CC	of diseases associated with inappropriate protein expression. The				
CC	polypeptides and nucleic acids may be used as nutrients or to modulate				
CC	cytokine and cell proliferation/differentiation activity and may also be				
CC	involved in modulation of the immune system. The cDNA sequences,				
CC	proteins, their agonists and/or antagonists exhibit haematopoiesis				
CC	regulating activity; tissue growth activity; activin/inhibin activity;				
CC	chemotactic/chemokinetic activity; haemostatic and thrombolytic				
CC	activity; receptor/ligand activity; anti-inflammatory activity;				
CC	haematopoiesis activity; cadherin/tumour suppressor activity; and/or				
CC	tumour inhibition activity. Included in the invention are probes				







Db 1385 GATGACTTCACAGTTTGTCCAGGTGCCCTGCCCTCCATGACACACCCCCCATTC 1444  
 QY 1385 TGGACAACAGAGGAGATACGCTGCTTAGAAGAGGCGGACTCTTAGATCCAGGATAG 1444  
 Db 1445 TGGACAACAGAGGAGATACAGCTGCTTAGAAGAGGCGGACTCTTAGATCCAGGATAG 1504  
 QY 1445 CCCYGTCTGGTCCAGTGTGGAGCTGCTCCATCCTCACTCCCTGAGGCGCAGGTG 1504  
 Db 1505 CCCCGTCTGGTCCAGTGTGGAGCTGCTCCATCCTCACTCCCTGAGGCGCAGGTG 1564  
 QY 1505 CTTGAGGCGCTGTCTGCCGAAAAAGCGGGCCCTGCATACACACTCTCAGAGCTGT 1564  
 Db 1565 CTTGAGGAGCTGTCTGCCGAAAAAGCGGGCCCTGCATACACACTCTCAGAGCTGT 1624  
 QY 1565 CAGGAAGCTGTCTGTCTCCAGACACGTCCTGCAGTTCCTCTCTACCGAGGCCCTT 1624  
 Db 1625 CAGGAAGCTGTCTGTCTCCAGACACGTCCTGCAGTTCCTCTCTACCGAGGCCCTT 1684  
 QY 1625 GCTKGGCTGTGATGCTGATTCACCAACAGCGGCTGGGCGGCTGCTTACAGGTGCTA 1684  
 Db 1685 GCTGCGCTGTGATGCTGATTCACCAACAGCGGCTGGGCGGCTGCTTACAGGTGCTA 1744  
 QY 1685 CGCCACTGTGGCTTCGGCTCCAGGACATGGCTGACTTTCCTCTCTGCTGCTGCTGCTG 1744  
 Db 1745 CGCCACTGTGGCTTCGGCTCCAGGACATGGCTGACTTTCCTCTCTGCTGCTGCTGCTG 1804  
 QY 1745 CGCTGGAGATCCGGAAGAGTTCCRAAGAGTGAAGGCGAGTACAGTGGCTTCAAGAG 1804  
 Db 1805 CGCTGGAGATCCGGAAGAGTTCCRAAGAGTGAAGGCGAGTACAGTGGCTTCAAGAG 1864  
 QY 1805 TCCTTACTGAGCCAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1853  
 Db 1865 TCCTTACTGAGCCAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1913  
 RESULT 5  
 AAC63693  
 ID AAC63693 standard; cDNA; 3540 BP.  
 AC AAC63693;  
 XX  
 DT 13-FEB-2001 (first entry)  
 XX  
 DE Rat P2X<sub>7</sub>/P2Z coding sequence.  
 XX  
 KW Rat; P2X<sub>7</sub>; neuroprotective; nootropic; antiinflammatory; antirheumatic;  
 KW antiarthritic; antibacterial; antiviral; antiallergic; cytostatic;  
 KW cardiant; cerebroprotective; immunosuppressive; P2Z; purinergic receptor;  
 KW nervous system disorder; chronic inflammation; Alzheimer's disease;  
 KW rheumatoid arthritis; amyloidosis; bacterial; viral; microbial infection;  
 KW haematopoietic system disorder; immune response; autoimmune disorder;  
 KW allergy; lymphoproliferative disorder; cardiac; cerebral ischaemia;  
 KW tuberculosis; ss.  
 XX  
 OS Rattus sp.  
 XX  
 PN US6133434-A.  
 XX  
 PD 17-OCT-2000.  
 XX  
 PF 28-APR-1997; 97US-0842079.  
 XX  
 PR 28-APR-1997; 97US-0842079.  
 XX  
 PA (GLAXO) GLAXO GROUP LTD.  
 XX  
 PI Buell GN, Kawashima E, Surprenant A;  
 XX WPI; 2001-006153/01.  
 DR P-PSDB; AAB28243.  
 XX  
 PT Mammalian purinergic receptor (P2X<sub>7</sub>) useful for screening for

PT modulators which are useful for treating arthritic, respiratory  
 PT disorders and neurodegenerative disorders, and to generate receptors  
 PT specific antibodies -  
 XX Claim 3; Fig 1B; 40pp; English.  
 XX  
 CC The present sequence is the coding sequence for rat purinergic receptor  
 CC P2X<sub>7</sub>/P2Z. This sequence can be used to treat disorders of the nervous  
 CC system, particularly diseases with a component of chronic inflammation,  
 CC such as Alzheimer's disease, diseases involving acute or chronic  
 CC inflammation such as rheumatoid arthritis, amyloidosis, bacterial, viral  
 CC and other microbial infections, disorders of the haematopoietic system  
 CC and immune response such as autoimmune disorders, allergies and  
 CC lymphoproliferative disorders, diseases involving apoptotic cell death,  
 CC such as cardiac and cerebral ischaemia and microbial infections,  
 CC particularly tuberculosis.  
 XX  
 SQ Sequence 3540 BP; 919 A; 958 C; 899 G; 764 T; 0 other;  
 Query Match 69.1%; Score 1281.2; DB 22; Length 3540;  
 Best Local Similarity 81.4%; Pred. No. 0;  
 Matches 1469; Conservative 11; Mismatches 324; Indels 0; Gaps 0;  
 QY 11 GAGGAGGCTGTCCACCATCGCGCTGCTGCAGCTGCAGTGTCTTCCAGTATGAGAC 70  
 Db 106 GAGTGAAGCTGTGCCATGCGGCTTGTGCGAGCTGGAAAGTGTCTTTCAGTATGAGAC 165  
 QY 71 GAACAAGTCACTCGGATCCAGAGATGAATATGACCACTTAAGTGGTGTCTTCCAGCT 130  
 Db 166 AAACAAGTCACTCGGATCCAGAGCTGAATATGACCACTTAAGTGGTGTCTTTCAGAT 225  
 QY 131 GATCATCTTTTCTACGTTTCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 190  
 Db 226 GACCGCTTTTCTTCTACGTTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 285  
 QY 191 GCCTGTCTACCTTCTGTGCACACCAAGGTGAAGGGGATAGCAGAGGTGAAGAGGAGAT 250  
 Db 286 GCCCTTATCAGCTCTGTGCACACCAAGGTGAAGGGGATAGCAGAGGTGAAGAGATGT 345  
 QY 251 CGYGGAGAAATGGAGTGAAGAGTGTGTGACAGTGTCTTGTGACCCGAGACTACACCTT 310  
 Db 346 CACGGAGGGGGGTGACGAAGTTAGTACACGCGATCTTCGACACGGCGGATACACCTT 405  
 QY 311 CCCTTTGAGGGGAACTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 370  
 Db 406 CCCTTTGAGGGGAACTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 465  
 QY 371 GCAGCGGTGTGTCCCGAGTATCCACCCGAGGAGCTTCTTCTCTGACCGAGGTG 430  
 Db 466 ACAGAGCTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 525  
 QY 431 TAAAGAGGATGGATGGAGCGCGAGAGCAAGAAATTCAGACCGGAGGTTGTAGTATTA 490  
 Db 526 TATAAAGGATGGATGGAGCGCGAGAGCAAGAAATTCAGACCGGAGGTTGTAGTATTA 585  
 QY 491 TGAAGGACACAGAGACCTGTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 550  
 Db 586 CGACAGAGAGAGAGAGACCTGTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 645  
 QY 551 GGCCCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 610  
 Db 646 AGCCCGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 705  
 QY 611 TATGACTTCCCGCGGCGGAGGAGTACACCGAGAGAAATTCCTGCGAGGTTTAAACATCAC 670  
 Db 706 TATGACTTCCCGCGGCGGAGGAGTACACCGAGAGAAATTCCTGCGAGGTTTAAACATCAC 765  
 QY 671 TTGTACTTCCACAGACTCAGATCCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 730  
 Db 766 TTGTACTTCCACAGACTTGAAGGAGTACACCGAGGAGTACACCGAGGAGTACATCTT 825  
 QY 731 CCGAGAGAGAGGAGTAAATTTTTCAGATGCGCAATTCAGGCGGAGTAAATTCAGGAGTAA 790



Db 182 AGGGTACCCAGGAACCTGACTCCGTGGTCACTCCGTTACGACCAAGGTCAGGCGGTGG 241  
Qy 232 CAGAGGTGAAGAGGAGATCGYGGGAATGAGGATGCAAGAAGTTGGTGCACAGTGTCTTTG 291  
Db 242 CTGTGACCAACACTCTTAACATGGATCCGGATCTGGGATGTGGGATTAATGTGTATC 301  
Qy 292 ACACGGCAGACTACACCTCCCTTTCAGGGGAACTCTTCTTCGTAAGGACAACTTTC 351  
Db 302 CAG-----CTCAGGAGGAAACTCCCTCTTCGTCATGACCAACGTGA 343  
Qy 352 TCAAAACAGAGGCCAGAGACGGGTGTGTCCCGAGTATCCACCCCGACGAGCGTCT 411  
Db 344 TCCTCACCATGAACACAGACAGGCGCTGTGCCCGGAGATTCAGATGGGACCACTGTGT 403  
Qy 412 GTTCTCTGACCGAGGTGTAAAGAGGATGATGGACCCGACAGACGAAGAAGTAATCAGA 471  
Db 404 GTAATACAGATGCGCAGCTGTACTGCGGCTCTGCCGACCCACACAGCAAGGAGTCTCAA 463  
Qy 472 CGGGAAGTGTGTAGTATGAGGGAACCAAGAACCTGTGAAGTCTCTGCTGGTGCC 531  
Db 464 CAGGAGGTGCTGTACTTCAACGGTCCGTCAGACGTGTGAGGTGGCGGCTGTGGCC 523  
Qy 532 CCATCGAGGAGTGAAGAGGCGCCCGGCTGTCTCTGAACAGTCCGGAACACTTCA 591  
Db 524 CGGTGGAGGTGACACACAGCTGCCACAACTGTCTTTTAAAGGCTGCAGAAACTTCA 583  
Qy 592 CTGTCTCATCAAGAACATATGAGCTTCCCGGCGCACAACTACACACGAGAAACATCC 651  
Db 584 CTCCTTTGTTGAAGAACATCTGTGTATCCCAAAATTAATTTCAAGAGAGGATATCC 643  
Qy 652 TGCAGGTTTAAACATCACT-----TGTACTTCCACAGACTCAGATCCAC 699  
Db 644 TTCACACATCCACACTACTTACTCAGTGTGCTATTTATGATCTAAACAGATCCCT 703  
Qy 700 AATGTCCATTTCCGACTAGGAGATCTTCCGAGAAACAGCGGTAATTTTTCAGATG 759  
Db 704 TCTGCCCATATTCCTGCTTGGCAAAATAGTGGAGACGCGAGCACACATTTCCAGGACA 763  
Qy 760 KGCATTCAGGGCGGAATAGGCAATGAGATCTACTGGGACTGCACTTACCTAGACGTT 819  
Db 764 TGGCGGTGGAGGAGGATCATGGGCATCCAGGTCAACTGGGACTGCACTTGGACAGAG 823  
Qy 820 GGTTCATCACTGCTCCCTCCCAATACAGTTTCCTTCGCTTGACGACCAAGACCAAG 879  
Db 824 CCGCTCCCTCTGTCTCCAGTACTCTTCGCGCTCGATACACGGGACGTGAGC 883  
Qy 880 TGTCTTTGACCTGGCTACACTTCAGATAGCCCAAGTACTACAGGAAACAATG--- 936  
Db 884 ACAAGTATCTCTGGCTACATTTTCAGGTTCGCAAGTACTACAGAGACCTTGGTGCA 943  
Qy 937 TTGAGAAACGGACTCTGATAAAGTCTTCGGGATCCGTTTGACATCTCTGTTTGGCA 996  
Db 944 AGCAGACGCAACCTCATCAGGCCATGGATCCGGTTCGACATCATTTGTTGGGA 1003  
Qy 997 CCGAGGAAATTTGACATTTCCAGCTGGTGTGTATCATCGGCTCAACCCCTCTCTACT 1056  
Db 1004 AGCAGGGAATTTGACATCATCCCACTATGATCAATCGGCTCTGCGCTGGCAGTCG 1063  
Qy 1057 TGGTCTGGCCCTGTGTTTCACTGCACTTCTCAIC 1091  
Db 1064 TAGGCATGGCAGCGCTGTGTGACATCATAGTC 1098

## RESULT 7

AAH25211  
ID AAH25211 standard; DNA; 1206 BP.  
XX  
AC AAH25211;  
XX  
DT 22-AUG-2001 (first entry)  
XX  
DE Nucleotide sequence of a human purinoreceptor P2X4.  
XX

Human; purinoreceptor; P2X2; P2X4; pain; neuroendocrine disease;  
auditory disease; vestibular disorder; ss.  
Homo sapiens.  
Key Location/Qualifiers  
CDS 21..1187  
/tag= a  
/product= "purinoreceptor P2X4"  
US6242216-B1.  
05-JUN-2001.  
13-NOV-1998; 98US-0191608.  
14-NOV-1997; 97US-0065822.  
20-AUG-1998; 98US-0137458.  
XX (ABBO ) ABBOTT LAB.  
Lynch KJ, Burgard EC, Metzger RE, Niforatos W, Touma EB;  
Van Biesen T;  
WPI: 2001-388837/41.  
P-PSDB; AAB84382.  
Isolated polynucleotides, used to produce P2X2 receptor polypeptides and  
identify potentially therapeutic compounds, encode a human P2X2  
receptor polypeptide -  
Example 4; Fig 11; 40pp; English.  
The specification describes nucleic acids encoding a functional human  
purinoreceptor polypeptides P2X2 and P2X4. P2X polypeptides and  
polynucleotides are used to identify modulators, which may be used to  
treat and prevent pain, diseases of the neuroendocrine system, and  
auditory and vestibular disorders. P2X and P2X polynucleotides are a  
source of probes and primers, which may be used to identify homologous  
sequences, for gene localisation studies, and for gene therapy purposes.  
The polynucleotides may also be used to produce the polypeptide  
recombinantly. The P2X polypeptides are used to arise antibodies, and  
to identify inhibitors. The present sequence encodes human P2X4.  
Sequence 1206 BP; 285 A; 335 C; 320 G; 266 T; 0 other;  
Query Match 12.7%; Score 235.4; DB 22; Length 1206;  
Best Local Similarity 54.3%; Pred. No. 3.5e-54;  
Matches 573; Conservative 5; Mismatches 441; Indels 36; Gaps 4;  
Qy 55 TTTTCCAGTATGAGACAGCAACAGTCACTCCGATCCAGACATGAATATGACACCATTA 114  
Db 55 TTTTCCAGTATGAGACAGCAACAGTCACTCCGATCCAGACATGAATATGACACCATTA 114  
Qy 115 AGTGTCTTCCAGTATGATCATCTTTTCTCTAGC---TTTCTTTTCTCTGTGTAGTAC 171  
Db 115 ACCGCGCGTCACTGCTCATCTCTGCTTACGTCATCGGTGGTGTGTGTGTGGGAAA 174  
Qy 172 AGCTGTACACCGGGAAGAGCCCTGTCAATCATCTTGTGACACCAAGGTAAGGGATAG 231  
Db 175 AGGGCTACAGGAACCTGACTCCGTGGTCTCCGTAGCAGGTCAGAGGTCAGGCGTGG 234  
Qy 232 CAGAGGTGAAGAGGAGATCGYGGGAATGAGTGAAGTGTGGTGCACAGTGTCTTTG 291  
Db 235 CTGTGACCAACACTCTTAACATGGATTCGGAATCTGGGATGTGGCGGATTAATGTATC 294  
Qy 292 ACACCGCAGACTACACCTTCCCTTTTCAGGGGAACTCTTTCTTCGTGTGATCAAACTTTC 351  
Db 295 CAG-----CTCAGGAGGAAACTCCCTCTTCGTCATGACCAACGTGA 336  
Qy 352 TCAAAACAGAGGCCAGAGACGCGGTGTGTCCGAGTATCCCAAGTATCCCAAGGAGCGTCT 411  
Db 337 TCTCATCATGAACACAGACAGCGGCTGTGCTCCCGGAGATTCAGATGCGACCATCTGT 396

	QY	412	GTTCCTCTCACCAGCGTTGTTAAATAAGGATGGATGGACCCGCAGAGACCAAGAAGTAATTGAGA	471
	Dd	397	GTAATAATCAGATGCCAGCTGTACTGCGGGCTCTTCCGGCACCCACAGACAAGGAGTGCTCAA	456
	QY	472	CCGGAAGGTGTACTGATRYATGAAGGAAACACAGAACCTGTGAAGTCTCTGCGCTGGTGCC	531
	Dd	457	CAGCGAGGTGCGTAGCTTTCAAGGGTCGCTCAGACAGGTGTGAGGTGGCGGGCTGGTGCC	516
	QY	532	CCATCAGGACGAGTGAAGAGAGGCCCGCCGGCCTGTCTCTTTGAACAGTGCAGAAAACACTTCA	591
	Dd	517	CGGTGGAGGATGACACACAGTGCACAACTGTCTTTTAAAGGCTGCAGAAACITCA	576
	QY	592	CTGTGTCATCAAGAAACAATATGCACTTCCCGGGCCAACATCATACACGAGAAACATPCC	651
	Dd	577	CTCTTTTGGTTAAGSACACATCTGTGTATCCCCAAATTTAATTTACGAAGAGGAATAPCC	636
	QY	652	TGCCAGGTTTTAAACATCACT-----TGTACCTTCCCAGAAGCTCAGAACTCCAC	699
	Dd	637	TTCCCAACATCACCACTACTTACCTCAAGTCGTGCTATTATGATGCTAAAAACAGATCCCT	696
	QY	700	AGTGTCCCAATTTTCGACTAGGAGACAATCTCCGAGAAACAAGCGATAAATTTTTCAGATG	759
	Dd	697	TCTGCCCCCATATTCGCTTTGGCAAAATATAGTGGAGAACGGAGACAGGTTTCCACGACA	756
	QY	760	KGSCAATTACAGSGCGGAATATGGGATTGGATCTACTGGACTGCACCTTAGACCGTT	819
	Dd	757	TGGCGGTGGAGGGAGGACATAGGGACATCCAGGTCAACTGGGACTGCAACCTTGGACACAG	816
	QY	820	GGTTCCATCACTGCCRTCCCAAAATACAGTTTCCRTGCGCTTGAGCAACAAGACCCACAAG	879
	Dd	817	OCGCGTCCCTGCTTGTCGCCAGGTACTCCTTCCGCGGCTCGATACAGGGACGTTGAC	876
	QY	880	TGTCCTGTATCOCTGGCTACAACTTCAGATACGCCAACTACTACAGGAAAACAATG---	936
	Dd	877	ACAACGTATCTCTGGCTACAAATTCAGGTTTGGCAAGTACTACAGAGACCTGGCTGGCA	936
	QY	937	TTGAGAAACGGAATCTGATAAAACCTCTGGGATCGGTTTGACATCCTGGTTTGGCA	996
	Dd	937	ACGAGACGCGACGCTCATCAAGGCTATGGCATCCGTTGCGATCATTTGTTTGGGA	996
	QY	997	CCGAGGAAAATTTGACATATTATCCAGCTGGTTGTGTACATCGGCTCAACCCCTCTCCTACT	1056
	Dd	997	AGGCAGGAAAATTTGACATCATCCCACATGNTCAACATCGGCTCTGGCCTGGCACATGC	1056
	QY	1057	TCGCTGTCGGCCRCCTGTGTTCATGCACTTCCTCATC	1091
	Dd	1057	TAGCATGTGGCAGCCGCTGTGTGCATCATATGTC	1091

## RESULT 8

RESOLUTION  
AAV09307

AAV09307  
ID AAV09307 standard; cDNA: 1759 BP.

XX  
XTAAV0  
AC

XX

DT 18-1

XX

DE  
Huma

XX

KW Bra:

KW  
human

XXV

SO  
HOM

XX 27

XX	30-APR-1996;	96WO-GE01034.
PF		
XX		
PR	30-APR-1996;	96WO-GE01034.
XX		
XX	(HUMA-) HUMAN GENOME SCI INC.	
PA	(SMTK ) SMITHKLINE BEECHAM PLC.	
XX		
PI	Carpenter DJ, Livingstone CD, McHALE MT, Tomlinson WJ;	
PI	Yi L;	
XX		
DR	WPI; 1997-549726/50.	
DR	P-PSDB; AAW47066.	
XX		
XX	DNA encoding human brain P2x receptors - used to develop products	
PT	for treating, e.g. brain or spinal cord traumas, infection,	
PT	inflammation and mood disorders	
XX		
XX	Claim 6; Fig 1; 31pp; English.	
XX		
XX	This cdna encodes a human brain P2X-1 receptor polypeptide. The P2X	
CC	receptor splice variants (P2X-1, P2X-2 and P2X-3 isoforms) can be	
CC	recombinantly expressed by a host cell genetically engineered with a	
CC	vector containing the encoding nucleic acids. The receptors can be used	
CC	to screen for their antagonists. The products can be used to identify	
CC	agents which modulate the activity of the receptors for use in clinical	
CC	conditions such as brain stroke, brain or spinal cord traumas, infection	
CC	and inflammation, cognitive disorders, epilepsy, affective and mood	
CC	disorders in general, including depression, various movement disorders	
CC	including parkinson's disease, Huntingtons Chorea and schizophrenia, as	
CC	well as those conditions that are associated with the development of	
CC	chronic or acute forms of pain, or cardiac anoxia. The products can also	
CC	be used for detection, production of antibodies and production of	
CC	transgenic animals as models for mutation and structure/activity	
CC	relationship evaluations as well as in drug screening.	
XX		
XX	Sequence 1759 BP; 402 A; 496 C; 480 G; 381 T; 0 other;	

Query Match 12.7%; Score 235.4; DB 18; Length 1759;  
Best Local Similarity 54.3%; Pred. NO. 4.3e-54;  
Matches 573; Conservative 5; Mismatches 441; Indels 36; Gaps 4



```

Db 777 TCTGCCCATATTCCTGCTTGGCAATCGTGGGGACGGGAGATACCTGCTCCAGAGA 836
QY 760 KGGCAATTCAGGGGGAATAATGCGCATTTGAGACTTACTGGGACTGCAACCTAGAACGTT 819
Db 837 TGGCAGTTTGGGGAGGCATCATGGGTATCCAGATCAAGTGGGACTGCAACCTGGATAG 896
QY 820 GGTTCATCACTGCTCCCAATACAGTTTCCCTGCGCTTGACGACAGACCAACG 879
Db 897 CGGCTTCCCTTGGCTGGCCAGATATTCCTTCGGGCGCTGGACACCGGAGCTGGAAC 956
QY 880 FTGCTTTACCTGCTTACACTTACATACAGTACGCAAGTACTACAGAG--AAACAATG 936
Db 957 ACAATGTCTCTGCTGGCTACATTTCAAGTTTGCAAGTACTACAGGACCTGGCGCA 1016
QY 937 TTGAGAAAGGACTGTGATAAGTCTTCGGGATCCGCTTTGACATCTGCTTTTGGCA 996
Db 1017 AAGACAGCGACACTACCAAGGCTAGCGCATCCGCTTGACATCATCTGTTGGAA 1076
QY 997 CGGAGGAAATTTGACATATCCAGCTGGTGTGTATCGGCTCAACCTCTCCNACT 1056
Db 1077 AGGCTGGAGTTTGACATATCCCTACATGATCAACGTGGCTGCTGGCGCTCC 1136
QY 1057 TCGGCTGGGCTGTGTTTCATCGACTTCCCTCATC 1091
Db 1137 TCGGGTGGGACGGTCTCTGTGTGACGTATGTC 1171

RESULT 10
AAD04979
ID AAD04979 standard; DNA; 1207 BP.
AC AAD04979;
XX
DT 17-JUL-2001 (first entry)
XX
DE Human purinergic receptor P2X4 receptor DNA.
XX
KW Human; purinergic receptor; P2X4; antidepressant; vulnerable; hypotensive;
KW anticonvulsant; antiinflammatory; therapy; nervous system disorder;
KW epilepsy; pain; depression; neurodegenerative disorder; cystic fibrosis;
KW irritable bowel disorder; reproductive system disorder; hypertension;
KW peripheral vascular disease; immune system disorder; chronic bronchitis;
KW premature ejaculation; asthma; neuromuscular disease; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 21..1186
FT /*tag= a
FT /product= "Human P2X4 receptor"
FT misc_feature 263
FT /*tag= b
FT /*note= "Represented in the specification as P"
XX
XX USG214581-B1.
XX
XX 10-APR-2001.
XX
XX 13-NOV-1998; 98US-0191136.
XX
XX 16-JAN-1998; 98US-0071298.
XX 16-JAN-1998; 98US-0071669.
XX 16-JAN-1998; 98US-0008185.
XX 16-JAN-1998; 98US-0008526.
XX
XX (ABBO ) ABBOTT LAB.
XX
XX Lynch KJ, Burgard EC, Van Biesen T;
XX WPI; 2001-315459/33.
XX
XX Novel isolated polynucleotide encoding human purinergic P2X3 receptor

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```

PT polypeptide useful for identifying potentially therapeutic compounds
PT that modulate or otherwise interact with P2X containing receptors -
XX
XX Example 11; Fig 10; 53pp; English.
XX
XX The present sequence is human P2X4 receptor DNA containing its open
XX reading frame with EcoRI restriction used for subcloning. P2X
XX receptors are ligand-gated ion channels while P2X receptors operate
XX generally through a G-protein coupled system. P2X purinoreceptor drugs
XX are potential therapeutic agents in several disorders including central
XX nervous system or peripheral nervous system conditions, e.g., epilepsy,
XX pain, depression, neurodegenerative disorders, disorders of the skeletal
XX muscle such as neuromuscular diseases, disorders of the reproductive
XX system, asthma, peripheral vascular disease, hypertension, immune system
XX disorders, irritable bowel disorder, premature ejaculation, cystic
XX fibrosis and chronic bronchitis. P2Y purinoreceptors mediate the activity
XX of extracellular nucleotide triphosphates to regulate chloride secretion
XX in human airway epithelia.
XX
XX Sequence 1207 BP; 285 A; 335 C; 320 G; 266 T; 1 other;

```

```

Query Match 12.6%; Score 233.8; DB 22; Length 1207;
Best Local Similarity 54.9%; Pred. No. 9.7e-54;
Matches 581; Conservative 4; Mismatches 432; Indels 41; Gaps 5;
QY 55 TTTTCCAGTATGAGACGACAAAGTCACTCGGATCCAGAGCATGAATTTATGGCACCATTA 114
Db 55 TGTTCGAGTACGACCGCGGCATCGTGTCTATCCGACGCGCAAGTGGGCTCATGA 114
QY 115 AGTGGTTCTTCCAGGTGATCATCTTTTCTACG---TTTGGCTTTGCTCTGGTGAAGTACA 171
Db 115 ACCGCGCGGTGCAACTGCTCATCTCTGGCTACGTCATCGGTGGTGTGTTGCTGGGAAA 174
QY 172 AGCTGTACGAGCGGAAGAGGCTGTATCATGTTCTGTGCACACCAAGTGAAGGGGATAG 231
Db 175 AGGGCTACCAAGAACTGACTCCGTGGTGGCTCCGTTACGACCAAGGTCAAGGGGTGG 234
QY 232 CAGAGGTGAAGAGGAGATCGTGGAGATGAGTGAAGAAGTTGGTGCACAGTGTCTTTG 291
Db 235 CTGTGACCAAC-----ACTTCTAACTTGGATTCGCGATCTGGG 274
QY 292 ACACCGCAGACTACACTTCC---CTTTGAGGGGAACTCTTTCTGTGTATGACAAACT 348
Db 275 ATGTGGGGATTTATGTATACAGCTCAGGAGGAAAACTCCCTCTGTCATGACCAACG 334
QY 349 TTTCTAAACAGAGCGCCAGAGCAGCGGTGTGTGTCGCCGATATCCACCGCAGGACGC 408
Db 335 TGATCTTCACCATGAAACCCAGACACAGGGCTGTGCCCCGAGATTCAGATCGCACCTG 394
QY 409 TCTGTTCTCTCTGACCGAGGTGTGTAAGAGGATGGATGGACCCGACAGACAAAGAACTC 468
Db 395 TGTGTAAATCAGATGCCAGCTGTACTGCGGCTCTCGCGSCACCCACAGCAAGGATCT 454
QY 469 AGACCGGAAGTGTGTAGTATGAGGAGAACAGAGACCTGTGAGTCTCTGCTGGT 528
Db 455 CAACAGCGCAGGTGCTGAGTCTTCAACGGGTCCGTCGTCGAGAGTGTGAGGTGGCGCTGT 514
QY 529 GCCCATCGAGCAGTGGAGAGGCCCGCGGCTGTCTCTTTGAACAGTCCGAAACT 588
Db 515 GCCCGTGGAGGATGACACACGTGCCACAACTGCTTTTAAAGGCTGCAGAAACT 574
QY 589 TCACTGTGCTCATCAAGAACAAATATCGACTTCCCGGCCACAACTACACACAGAAACA 648
Db 575 TCACTCTTTTGGTTAAGAACAACTCTGTTATCCCAATTTAATTTACGCAAGGAATA 634
QY 649 TCCTGCCAGGTTTAAACATCACT-----TGTACCTTCCACAGACTCAGATC 696
Db 635 TCCTTCCCAACATCACTCACTTACCTCAAGTCTGTCATTTATGATGCTAAAAAGATC 694
QY 697 CACAGTGTCCCATTTTCCGACTTAGGAGACATCTTCCGAGAAACAGGCGATATATTTTCAG 756
Db 695 CCTTCTGCCCATATTCCTGCTCTTGGCAAAATGATGGAGAACGACGAGACGCTTTCAGG 754

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Qy 1078 TCGACTTCTCATC 1091  
 Db 1119 GTGACATCATGTC 1132

# RESULT 12 ABK84338

ID ABK84338 standard; cDNA; 2633 BP.

XX

AC ABK84338;

XX

DT 14-AUG-2002 (first entry)

XX Human cDNA differentially expressed in granulocytic cells #909.

XX Human; ss; granulocytic cell; DNA chip; bacterial infection;

KW viral infection; parasitic infection; protozoal infection;

KW fungal infection; sterile inflammatory disease; psoriasis;

KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;

KW cardiac reperfusion injury; renal reperfusion injury; ARDS;

KW adult respiratory distress syndrome; inflammatory bowel disease;

KW Crohn's disease; ulcerative colitis; periodontal disease;

KW granulocyte activation; chronic inflammation; allergy.

XX Homo sapiens.

OS

PN W0200228999-A2.

XX

PD 11-APR-2002.

XX

PF 03-OCT-2001; 2001WO-US30821.

XX

PR 03-OCT-2000; 2000US-237189P.

XX

PA (GENE-) GENE LOGIC INC.

XX

PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;

XX

DR WPI; 2002-435328/46.

XX

XX

PT Detecting granulocyte activation by detecting differential expression

PT of genes associated with granulocyte activation, which serves as

PT diagnostic markers that is useful for monitoring disease states and

PT drug toxicity

XX

PS Claim 1; SEQ ID No 909; 114pp; English.

XX

CC The invention relates to detecting (M1) granulocyte (GC) activation

CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by

CC DNA chip analysis as given in the specification, and comparing

CC the expression level to an expression level in an unactivated

CC GC, where differential expression of Gs is indicative of GCA.

CC Also included are modulating (M2) GA by contacting GC with an agent

CC that alters the expression of at least one gene in Gs; (2) screening (M3)

CC for an agent capable of modulating GCA or an inflammation (especially

CC chronic) in a tissue, an allergic response in a subject, exposure of a

CC subject to a pathogen or sterile inflammatory disease using the

CC gene expression profile; (3) detecting (M4) an inflammation (especially

CC chronic) in a tissue, an allergic response in a subject, exposure of a

CC subject to a pathogen or sterile inflammatory disease, by detecting the

CC level of expression in a sample of the tissue of gene(s) from Gs, where

CC the level of expression of the gene is indicative of inflammation;

CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,

CC or sterile inflammatory disease, by contacting a tissue having

CC inflammation with an agent that modulates the expression of gene(s)

CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for

CC modulating GA; M3 is useful for screening an agent capable of modulating

CC reperfusion injury, ARDS, adult respiratory distress syndrome,  
 CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,  
 CC periodontal disease; also bacterial infection, viral infection and M5 is  
 CC parasitic infection, protozoal infection, fungal infection and M5 is  
 CC useful for treating one of the above conditions. The present  
 CC sequence represents a gene differentially expressed in granulocytes.  
 CC Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX

XX

SQ Sequence 2633 BP; 582 A; 804 C; 701 G; 546 T; 0 other;

Query Match 11.0%; Score 203.8; DB 24; Length 2633;

Best Local Similarity 54.8%; Pred. No. 2.5e-45;

Matches 447; Conservative 5; Mismatches 342; Indels 21; Gaps 2;

Qy 285 GTCTTTGACACCGCAGACATACACCTTCCTTCAGGGGAACTCTTCTCGTGATGACA 344

Db 446 GTCTGGGATGGCTGACTACGCTTCCAGCCAGGGGGACAACTCTCTGTGTGTCATG 505

Qy 345 AACTTTCTCAAAACAGAGGCCAAGAGCGGTTGTCCCGAGTATCCACCCCGAGG 404

Db 506 ACCAATTTTCATCGTACCCCGGAGCAGACTCAAGGCTACTGGCAGAGCACCACGAAGGG 565

Qy 405 AGGCTCTGTTCTCTGACCGAGGTTGTAAAGAGGATGGATGACCCGACAGCAAGGA 464

Db 566 GGCATATGCGAAGAGACAGAGTGGCTGTACCCCTGGGAGGCCAAGAGAGCCCAAGGC 625

Qy 465 AATCAGACCGGAAAGTGTGTAGTATYANGAAGGGAACCAAGAACCTGTGAAGTCTCTGCC 524

Db 626 ATCCGACGGGCAAGTGTGTGGCTTCAACGACACTGTGAAGACGTGTGAGATCTTTGGC 685

Qy 525 TGGTGGCCCTATCGAGGACGTGAGAGAGCCGCCCGGCTGCTCTTTGAACAGTGGCGAA 584

Db 686 TGGTGGCCCTGAGGAGTGGATGACGACATCCCGGCGCTTCTCTCCGAGAGGCGGAG 745

Qy 585 AACTTCACTGTGCTCATCAAGAACATATGACTTCCCGGCGCACAACTACACACAGAGA 644

Db 746 AACTTCACTCTTTATCAAGACAGACATAGCTTTCCAGCGCTTCAAGGTCAACAGCGCG 805

Qy 645 AACTTCTCCGAGGTTTAAA-----CATCACTTGTACCTTCCCAAGACTCAG 692

Db 806 AACCTGTGGAGAGGTGAATGCTGCCACATGAAGACCTGCTCTTTCACAGACCCCTG 865

Qy 693 AATCCACAGTGTCCCATTTTCCGACTAGGACACTTCCGAGAACAGGCGGATATTTT 752

Db 866 CACCCCTGTGGCGGCAATTCAGGCGGGAATAATGGCAATTGAGATCTACTGGGACTGCAACTA 812

Qy 753 TCAGATGKGGCAATTCAGGCGGGAATAATGGCAATTGAGATCTACTGGGACTGCAACTA 812

Db 926 AGCACCTGTGGAGAGGTTGGAGTGGTGGCATCACCATGACTGGCAGTGTGACCTG 985

Qy 813 GACCGTTGGTTCATCATCTGCGCTCCCAATPACAGTTTCCTCGGCTTGACGACAGAAC 872

Db 986 GACTGGCACGTACGGCACTGACAGACCCATCATGAGTTCATGGCTGTACGAGAGAAA 1045

Qy 873 ACCAAGGTGCTTGTACCTGGCTACAACTTCAGATAGCAGTACCAAGTACTACAGGAAAC 932

Db 1046 A-----ATCTCTCCCGAGGCTTCACTTCAAGTTGCGAGGACTTTGTGAGAAC 1096

Qy 933 AATGTTGAGAAAGGACTCTGATAAAAGTCTTGGGATCGGTTTGACATCTCTGTTTTT 992

Db 1097 GGGACCAACTACCTTCACTCTTCAAGTGTGTTGGGATTCGCTTTGACATCTCTGTTGAC 1156

Qy 993 GGCACCGGAGGAAAATTGACATTTATCCAGCTGGTGTGTACATGGCTCAACCTCTCC 1052

Db 1157 GCGAGGCGCGGAGTTTGTACATCATCTCTACATGACCAACCATCGCTCGTGAATTGGC 1216

Qy 1053 TACTTGGTGTGTCGCTGTGTTTCATGACTTCTCT 1087

Db 1217 ATCTTTGGGGTGGCCACAGTCTCTCTGTGACCTGCT 1251



Db 1046 A-----ATCTCTCCCGAGGCTTCAACTTCAGGTTTCCAGGACACTTTGTGGAGAC 1096  
 QY 933 AATGTTGAGAAACGAGCTCTGAPAAAGTCTCGGATCGGTTTGTGACATCCTGGTTTTT 992  
 Db 1097 GGGACCAACTACCGTCACTCTTCAAGGTGTTTGGGATTGCTTTGACATCCTGGTGGAC 1156  
 QY 993 GGCACCGGAGAAATTTGACATTATTCAGCTGCTTGTGTGATCATCGACCTCTCC 1052  
 Db 1157 GGCAGGCGGGAGATTTGACATCATCTCCATGACACCAACATCGGCTCTGGAATTGGC 1216  
 QY 1053 TACTTCGCTCGCCCTGCTGTGTCATCGACTTCCT 1087  
 Db 1217 ATCTTTGGGGTGGCCACAGTCTCTGTGAOCTGCT 1251

## RESULT 14

AAT33855

ID AAT33855 standard; cDNA; 2643 BP.

XX AC AAT33855;

XX DT 23-NOV-1996 (first entry)

XX DE Human urinary bladder P2x receptor cDNA.

XX KW ATP P2x receptor; purinoceptor; ligand-gated ion channel; agonist;

XX KW antagonist; epilepsy; cognition; emesis; pain; asthma;

XX KW peripheral vascular disease; hypertension; irritable bowel syndrome;

XX KW premature ejaculation; cystitis; therapy; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 174..1373

XX FT /\*tag= a

XX PN W09533048-A2.

XX PD 07-DEC-1995.

XX PP 24-MAY-1995; 95WO-EP01968.

XX PR 09-FEB-1995; 95GB-0002480.

XX PR 27-MAY-1994; 94GB-0010664.

XX PA (GLAXO) GLAXO GROUP LTD.

XX PI Buell GN, Valera S;

XX PT WPI; 1996-030561/03.

XX DR P-PSDB; AAW04218.

XX PT DNA encoding ATP P2x receptors of the purinoceptor family - for

XX PT screening cpds. useful in treating epilepsy, cognition, emesis,

XX PT pain, asthma, peripheral vascular disease, hypertension, etc.

XX PS Claim 1; Fig 4; 82pp; English.

XX CC A cDNA clone (AAT33855) codes for the human urinary bladder P2x

XX CC receptor (AAW04218), a ligand-gated ion channel that opens upon

XX CC binding of extracellular ATP. It was isolated from a bladder

XX CC cDNA library using a rat smooth muscle P2x receptor probe.

XX CC Rat vas deferens, superior cervical ganglion and dorsal root

XX CC ganglion P2x receptor cDNAs (AAT33852-54) have also been isolated.

XX CC These cDNAs can be used to produce recombinant P2x receptors in

XX CC host, esp. mammalian, cells for use in screening (ant)agonist

XX CC cpds.

XX SQ Sequence 2643 BP; 607 A; 794 C; 701 G; 541 T; 0 other;

XX Query Match 11.08; Score 203.8; DB 17; Length 2643;

XX Best Local Similarity 54.88; Pred. No. 2.6e-45;

XX Matches 447; Conservative 5; Mismatches 342; Indels 21; Gaps 2;

QY 285 GTCTTTGACACCGCAGACTACACCTTCCCTTTCAGGGGAACTCTTCTTCGTGATGACA 344  
 Db 423 TCTTGGGATGTGCTGCTAGCTTCTCCAGCCCGGGGAACTCTTCTTCGTGGTCAATG 482  
 QY 345 AACTTTCTCAAAACAGAGGCAAGAGCAGCGGTGTTGTCCCGAGATCCCAACCCGAGG 404  
 Db 493 ACCAATTTCACTCGTACCCCAAGCAGACTCAAGGCTACTGGCAGAGACCCAGAGGG 542  
 QY 405 ACGTCTGTTCCTCTGACCGAGGTTGTAAAGAGGATGATGGACCCGAGACCAAGGA 464  
 Db 543 GGCATATGCAAGGAAGAGAGTGGCTGTACCCCTGGGAGGCCAAGAGGAAGGCCAAGGC 602  
 QY 465 ATTACAGACCGGAGGTGTGTATGATGAGGGAACACAGAGACTGTGAGTCTCTGCC 524  
 Db 603 ATCCGCACGGGCAAGTGTGTGGCCTTCAACGACACTGTGGAAGCGTGTGAGATCTTTGGC 662  
 QY 525 TGGTCCCGCATCGAGGAGTGGAGAGGCCCCCGGCTGTCTTCTTGAACCTGGCCGAA 584  
 Db 653 TGGTCCCGCTGGAGGTGGATGACGACATCCCGGCCCTGCCCTTCTCCGAGAGGCCGAG 722  
 QY 585 AACTTCACTGTCTCATCAGACAAATATGATGATTTCCCGGGCCACACTACACACAGAA 644  
 Db 723 AACTTCACTCTTTTCATCAAGAACAGCATCAGCTTTCCACGCTTCAAGGTCAACAGGCG 782  
 QY 645 AACATCTCGCCAGGTTTAA-----CATCACTTGTAACCTTCCACAGACTCAG 692  
 Db 793 AACTGTTGAGAGAGTGAATGCTGCCACATGAAGACCTGCCCTTTCACAGACCCCTG 842  
 QY 693 AATCCAGTGTCCCATTTTCCGACTAGGAGACATCTCCGAGAAACAGGCGATAATTT 752  
 Db 843 CACCCCTGTGCCCATCTCTCCAGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 902  
 QY 753 TCAGATGKGCATTCAGGCGGGAATATGGGATTCAGATCTACTGGGACTGCACACCTA 812  
 Db 903 AGCACCCCTGGCTGAGAAGGGTGGAGTGGTGGCATCACCATCGACTGCTGACCTG 962  
 QY 813 GACCGTTGGTTCCATCACTGCTCCCAATACAGTTTCCRTCCGCTTGACACAGAAC 872  
 Db 963 GACTGGCAGCTGACGGCAGCTGACAGCCCATCTATGACTTCCATGGCTGTACGAGAGAA 1022  
 QY 873 ACCAAGCTGTCTTGTACCTGGCTGATCACTTCACTGATGAGCCCAAGTACTACAGGAAAC 932  
 Db 1023 A-----ATCTCTCCCGAGGCTTCAACTTCAGGTTTTCAGGCACTTTTGGGAGA 1073  
 QY 933 AATGTTGAGAAACGAGCTCTGATATAAGTCTTCGGGATCCGTTTGTGACATCGCTGTTTTT 992  
 Db 1074 GGGACCAACTACCGTCACTCTTCAGGTGTTTGGGATTCGCTTTGACATCCTGGTGGAC 1133  
 QY 993 GGCACCGGAGGAAATTTGACATTATCCAGCTGGTTGTGTATCATCGGCTCAACCTCTCC 1052  
 Db 1134 GGCAGCGCGGGAAGTTTGACATCATCCTACATGACCAACCATCGGCTCTGGAATTGGC 1193  
 QY 1053 TACTTGGCTGCGCCCTCTGTGTTCATCGACTTCCT 1087  
 Db 1194 ATCTTTGGGGTGGCCACAGTCTCTCTGTGAOCTGCT 1228

## RESULT 15

AAV89619

ID AAV89619 standard; cDNA; 294 BP.

XX AC AAV89619;

XX DT 15-FEB-1999 (first entry)

XX DE EST clone C0390.

XX KW Human; secreted protein; expressed sequence tag; EST; haematopoiesis;

XX KW tissue growth; activin; inhibitor; chemotaxis; chemokinesis; haemostatic;

XX KW receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;

XX KW gene therapy; ss.

XX XX

```
OS Homo sapiens.
XX
XX WO9845436-A2.
XX
XX PD 15-OCT-1998.
XX
XX PF 10-APR-1998; 98WO-US06955.
XX
XX PR 10-APR-1997; 97US-0838821.
XX
XX PA (GENY ) GENETICS INST INC.
XX
XX PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;
XX PI Racie LA, Spaulding V, Treacy M;
XX
XX DR WPI; 1999-070077/06.
XX
XX PT New polynucleotides encoding human secreted proteins - derived from
XX PT e.g. human blood, kidney, foetal lung, placenta, testes, brain,
XX PT ovary, pituitary, retina and colon cDNA libraries.
XX
XX PS Claim 1; Page 276; 618pp; English.
XX
XX CC The present sequence represents a human expressed sequence tag (EST).
XX CC The polynucleotide, which is a secreted EST, and the encoded protein
XX CC are predicted to have useful biological activities which would make
XX CC them suitable for treating, preventing or ameliorating medical
XX CC conditions in humans and animals, although no supporting data is
XX CC given. Suggested activities include nutritional activity, immune
XX CC stimulating or suppressing activity, haematopoiesis regulating
XX CC activity, tissue growth activity, activin/inhibin activity,
XX CC chemotactic/chemokinetic activity, haemostatic and thrombolytic
XX CC activity, receptor/ligand activity, anti-inflammatory activity,
XX CC cadherin/tumour invasion suppressor activity, tumour inhibition
XX CC activity. The polynucleotide may also be useful for gene therapy.
XX
XX SQ Sequence 294 BP; 81 A; 72 C; 68 G; 73 T; 0 other;

Query Match 10.6%; Score 196.4; DB 20; Length 294;
Best Local Similarity 98.5%; Pred. No. 9.1e-44;
Matches 197; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 576 AGTCCGAAACCTCAGTGTCTCATCAAGAACAAATATCGACTTCCCGGCGCAACTAC 635
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
30 AGTCCGAAACCTCAGTGTCTCATCAAGAACAAATATCGACTTCCCGGCGCAACTAC 69
QY 636 ACCACGAGAAACATCTCTGCTCATCAAGAACAAATATCGACTTCCCGGCGCAACTAC 695
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
90 ACCACGAGAAACATCTCTGCTCATCAAGAACAAATATCGACTTCCCGGCGCAACTAC 149
QY 696 CCACAGTGTCCCATTTTCCGACTAGGACATCTTCCGAGAAACAGGCGAATTTTCA 755
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
150 CCACAGTGTCCCATTTTCCGACTAGGACATCTTCCGAGAAACAGGCGAATTTTCA 209
QY 756 GATGCGCAATTCAGGCGG 775
Db ||||||||||||
210 GATGCGCAATTCAGGCGG 229
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Search completed: July 18, 2003, 20:53:32  
Job time : 455 secs

Result No.	Query			ID	Description
	Score	Match	Length		
1	1843.8	99.5	1853	US-08-842-079-19	Sequence 19, Appl
2	1281.2	69.1	3540	US-08-842-079-16	Sequence 16, Appl
3	237	12.8	1762	US-08-742-621-2	Sequence 2, Appl
4	235.4	12.7	1206	US-09-191-608-21	Sequence 21, Appl
5	234.6	12.7	1997	US-08-750-134A-6	Sequence 6, Appl
6	234.6	12.7	1997	US-09-363-745-6	Sequence 6, Appl
7	203.8	11.0	2643	US-08-750-134A-10	Sequence 10, Appl
8	203.8	11.0	2643	US-09-363-745-10	Sequence 10, Appl
9	159.6	8.6	1837	US-08-750-134A-4	Sequence 4, Appl
10	159.6	8.6	1837	US-09-363-745-4	Sequence 4, Appl
11	148.4	8.0	1272	US-09-191-136-13	Sequence 13, Appl
12	148	8.0	1243	US-09-191-136-15	Sequence 15, Appl
13	140.2	7.6	1753	US-08-750-134A-8	Sequence 8, Appl
14	140.2	7.6	1753	US-09-363-745-8	Sequence 8, Appl
15	140	7.6	1421	US-09-191-608-14	Sequence 14, Appl
16	140	7.6	1436	US-09-191-608-13	Sequence 13, Appl
17	138.4	7.5	1349	US-09-191-608-15	Sequence 15, Appl
18	135.6	7.3	1499	US-09-191-608-16	Sequence 16, Appl
19	109.4	5.9	1293	US-09-381-681-1	Sequence 1, Appl
20	109.4	5.9	1697	US-09-381-681-2	Sequence 2, Appl
21	107.8	5.8	1360	US-09-191-136-30	Sequence 30, Appl
22	96.8	5.2	878	US-07-915-934-3	Sequence 3, Appl
23	96.8	5.2	878	US-08-325-743-3	Sequence 3, Appl
24	94.8	5.1	531	US-09-191-608-8	Sequence 8, Appl
25	44.6	2.4	7218	US-08-232-463-14	Sequence 14, Appl
26	42.4	2.3	2543	US-08-555-6659-11	Sequence 11, Appl
27	42.4	2.3	2543	US-09-073-663-11	Sequence 11, Appl





MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE: CONSENSUS  
US-08-742-621-2

Query Match 12.8%; Score 237; DB 2: Length 1762;  
Best Local Similarity 54.4%; Pred. No. 7.9e-60;  
Matches 574; Conservative 5; Mismatches 440; Indels 36; Gaps 4;

```
QY 55 TTTTCAGTATGAGACGAAAGATCCTCGGATCCAGAGCATGAATATGACACCATTA 114
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 62 TGTTCAGTACGACGCGCGCATGCTCTATCCGACGCGCAAGTGGGGCTCAGA 121

QY 115 AGTGGTCTTCACGCGATCATCTTTTCTAG---TTTGGTTTGTCTGGTGTGACA 171
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 122 ACCGGCGCGTCAACTCTCATCTGGCCCTAGTCTCATGGGTGGTGTGTGGGAAA 181

QY 172 AGTGTGTACAGCGGAAAGCCTGTCTCATCTGTCTGCACACCAAGGTGAAGGGATAG 231
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 182 AGGCTACAGGAACCTGACTCGTGTCTAGTCTCGTTACACCAAGGTCAAGGGCGTGG 241

QY 232 CAGAGTGAAAGAGAGATCGYGGAGATGGAGTGGTGCACAGTCTCTTTG 291
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 242 CTGTGACCAACTCTTAACCTTGGATTCCGGATCTGGGATGGGGATTATGTGATAC 301

QY 292 ACACCGCAGATACACCTTCCCTTTCAGGGGAACCTTCTTCGTGTGATGACAAACTTC 351
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 302 CAG-----CTCAGGAGGAAACTCCCTCTTCTGTCATGACACACCTGTA 343

QY 352 TCAAAACAGAGGCGCAAGACGCGTGTGTCCCGAGTATCCACCGCAGGACGCTCT 411
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 344 TCCTCACCATGACACACAGCGGCTGTGCCCGAGATTCAGATGCGACCATGTGT 403

QY 412 GTTCTCTGACGAGGTGTAAAGAGGATGGACCCGCGAGAGCAAGGAATTCAGA 471
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 404 GTAAATCAGATCGCAGCTGACTCCGGCTCTGCGGCACCCACAGCAAGGCTCA 463

QY 472 CGGAGGTGTGTAGTATGAGGAAACAGACAGACCTGTGAGTCTGCTCTGCTGCC 531
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 464 CAGGAGGTGGCTGACTTTCAAGCGGTCTGACAGCTGTGAGGTGGGGCTGGTGCC 523

QY 532 CCATCGAGCAGTGTGAAGAGGCCCCCGGCTGCTCTTGAACAGTGTGCGGAAACTTCA 591
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 524 CGGTGAGGATGACACACAGCTGCCACACTGCTTTTAAAGGCTGCAAGAAACTTCA 583

QY 592 CTGTGCTCATCAGAACAAATAGCACTTCCCGGCCCACTACACACAGAGAAACATCC 651
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 584 CTCTTTTGTAAAGAACAACTCTGTATCCCAAAATTTAATTTACGACAGAGGAATATCC 643

QY 652 TGCAGGTTTAAACATCACT-----TGTACCTTCCACAGACTCAGATCCAC 699
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 644 TTCCCAACATCACCCTACTTACTCACTGCTGCTATTTATGATGCTTAAACAGATCCCT 703

QY 700 AGTGTCCCATTTCCGACTAGGACATCTCCGAGAACAGCGGATTAATTTTCAGATG 759
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 704 TCTGCCCATATTCGGTCTTGGCAAAATAGTGAGAACGAGGACAGTTTCCAGGACA 763

QY 760 KGCATTCAGCGCGGATATGGGATTTGAGATCTCTGGGACTGCACTTAGACCGTT 819
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 764 TGGCCGTGGAGGAGGATATGGGATCCAGGTCACTGGGACTGCACTTGGACAG 823

QY 820 GGTTCATCATCTGCCCTCCAAATACAGTTTCCRCCTTGTGAGCAAGACACCAAG 879
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 824 CCCTCTCTCTGCTGCGCAGGTACTCTCTCCCGCGCTCGATACAGGGAGTTGAGC 883

QY 880 TGTCTTTGACCTTGGCTTACACTTTCAGATAGCCCAAGTACTACAGGAAACAAATG--- 936
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 884 ACAACGTATCTCTGGCTTACAAATTTCAAGTTTGGCAAGTACTACAGAGACTGGCTGSCA 943

QY 937 TTGAGAAACGGGACTCTGATAAAGTCTTCGGGATCCGTTTTCAGATCCCTGGTTTGGCA 996
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 944 ACAGAGGCGCAGCTCATCAAGGCTATGGCATCCGCTTCGACATCATTTGTGTGGGA 1003
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QY 997 CCGAGGAGAAATTTGACATTTATCCAGCTGGTTGTGTACATCGCTCAACCCCTCTCTACT 1056
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Db 1004 AGGCAGGAAATTTGACATTTATCCACCATATGATCAACATCGCTCTGGCTGGCACTGC 1063

QY 1057 TCGGTCTGGCCTGTGTCTCATCGACTTCCCTCANC 1091
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Db 1064 TAGCATGGCAGCGCTGTGTGTGACATCATAGTC 1098
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## RESULT 4

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US-09-191-608-21
; Sequence 21, Application US/09191608
; Patent No. 6242216
; GENERAL INFORMATION:
; APPLICANT: Lynch, Kevin J.
; APPLICANT: Burgard, Edward C.
; APPLICANT: Metzger, Randy E.
; APPLICANT: Niforatos, Wende
; APPLICANT: Touma, Edward B.
; APPLICANT: Van Biesen, T.
; TITLE OF INVENTION: Nucleic Acids Encoding a Functional
; TITLE OF INVENTION: Human Purinoreceptor P2X2 and P2X4 And Methods Of Production
; FILE OF INVENTION: And Use Thereof
; FILE REFERENCE: 6394.US.P1
; CURRENT APPLICATION NUMBER: US/09/191,608
; CURRENT FILING DATE: 1998-11-13
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 1206
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-191-608-21
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Query Match 12.7%; Score 235.4; DB 4: Length 1206;  
Best Local Similarity 54.3%; Pred. No. 1.9e-59;  
Matches 573; Conservative 5; Mismatches 441; Indels 36; Gaps 4;

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QY 55 TTTTTCAGTATGAGACGAAAGATCCTCGGATCCAGAGCATGAATATGACACCATTA 114
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 55 TGTTCAGTACGACACGCGCGCATGCTGCTCATCCGACGCGCAAGTGGGGCTCATGA 114

QY 115 AGTGTGTCTTCCAGCTGATCATCTTTTCTAG---TTTGGTTTGTCTGGTGTGAGGACA 171
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 115 ACGGCGCGTCAACTGCTCTCTCTGGCTCTAGCTCATCGGTGGTGGTGTGTGTGGGAAA 174

QY 172 AGCTTACACGCGGAAAGACCTGTCTCATAGTTCTGTGCACCAAGGTGAAGGGGATAG 231
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 175 AGGGCTACCGAGAAACTGACTCCGTGTGAGTCCGTTCAGCAAGGTCAAGGGCGTGG 234

QY 232 CAGAGTGAAGAGAGAGATCGGAGATGGAGTGAAGAGTGGTGCACAGTGTCTTTG 291
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 235 CTGTGACCAACACTTTTAAACTTGGATTCCGGATCTGGGATTTGATGTATGATAC 294

QY 292 ACACGCGAGACTACACCTTCCCTTTTCAGGGGAACTCTTTTCGTGATGACAAACTTTC 351
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 295 CAG-----CTCAGGAGGAAACTCCCTTCTGTCATGACCAACGTGA 336

QY 352 TCATAACAGAGGCGCAAGACAGCGGTGTGTCCGAGTATCCACCCCGCAGGACGCTCT 411
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 337 TCCTCACCATGAACAGACACAGGGCGTGTGCCCGAGATTCAGATGCGGACACTGTGT 396

QY 412 GTTCTCTGACCGAGTGTCTTAAAGAGGATGGATGGACCCCGCAGACCAAGAAATCAGA 471
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 397 GTAAATCAGATGCCAGTGTACTTGCCTGTGCGGCTTGGCGGCCACACAGCAAGGCTCAA 456

QY 472 CCGGAGGTGTGTAGTATGAGGAGAACAGAAAGACTGTGAAGTCTCTGCTGGTGGCC 531
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 457 CAGGACAGTGGCTAGCTTTTCAAGGGTCCGTCAGACAGTGTGTGAGGTGGCGGCTGGTGGCC 516

QY 532 CCATCGAGGCGAGTGAAGAGGCGCCCGCGCTGTCTTGAACAGTGCAGGAAACTTCA 591
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 517 CGGTGGAGGATGACACACACACGTCGCCAACCTGCTTTTAAAGGCTGCAGAAATTC 576  
QY 592 CTGTCGTATCAGAACAAATATCAGCTTCCCGGCCACAACTACACACAGAGAAATCC 651  
Db 577 CTCTTTGTTGAAGAACAACTATCGTATCCCAATTTAAATTCAGCAAGAGGAATCC 636  
QY 652 TGGCAGGTTTAAACATCACT-----TGTACCTTCCACAAGACTCAGAACTCCAC 699  
Db 637 TTCCACATACACACTACTTACCTCAAGTCGTGCATTAATGATGCTTAAACAGATCCCT 696  
QY 700 AGTGTCCCATTTTCCGACTAGAGACATCTCCGAAACACAGCGCAATAATTTTCAGATG 759  
Db 697 TCTGCCCATATATTCGTCTTGGCAAAATAGTGAGAAACGACGACACGGTTTCCAGSACA 756  
QY 760 KSGCAATTGAGGGCGGAATATGCGCAATTCAGATCTACTGGGACTGCAACTAGACCGTT 819  
Db 757 TGGCCGTGAGGGAGGCAATCATGGGCATCCAGGTCACTGGGACTGCAACTGGACAGAG 816  
QY 820 GGTTCATCACTGCGCTTCCCAATACAGATTTCCCTCGCTTGAACAGACACCAACG 879  
Db 817 CGCCCTCCCTGCTTGCCTGCGAGGTACTCTTCCGCGCTCGATACAGGAGCTTGAC 876  
QY 880 TGTCCCTGACCTGGCTACAACTCAGATACGCCAAGTACTACAGGAAACAAATG--- 936  
Db 877 ACAACGTATCTCTGCTACAAATTCAGTTTTGCCAAGTACTACAGAGACCTGGCTGGCA 936  
QY 937 TTGAGAAACGGACTCTGATAAAGCTTTCGGGATCCGTTTGACATCTGTTGGTGGCA 996  
Db 937 ACAGAGCGGACGCTCATCAAGGCTTATGGCATCCGCTTGCATCATATTTGTTGGGA 996  
QY 997 CGGAGGAAATTTGACATTTCCAGCTGGTTGTGATATCGGCTCAACCTCTCTACT 1056  
Db 997 AGCAGGGAATTTGACATATCCACATATCCGCTATGATCAATCGGCTGCGCTGGCACTGC 1056  
QY 1057 TCGGCTGGCCTCTGTTTAPCGACTTCCTCATC 1091  
Db 1057 TAGGCATGGCAGCGCTGCTGTGACATCATAGTC 1091

RESULT 5

US-08-750-134A-6  
; Sequence 6, Application US/08750134A  
; Patent No. 5985603  
; GENERAL INFORMATION:  
; APPLICANT: VALERA, SOLEDAD  
; APPLICANT: BUELL, GARY  
; TITLE OF INVENTION: P2X RECEPTORS (PURINOCEPTOR FAMILY)  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHUYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/750,134A  
; FILING DATE: 22-JAN-1997  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CRAWFORD, ARTHUR C.  
; REGISTRATION NUMBER: 25,327  
; REFERENCE/DOCKET NUMBER: 1430-116  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 816-4006  
; TELEFAX: (703) 816-4100  
; INFORMATION FOR SEQ. ID NO. 6:  
; SEQUENCE CHARACTERISTICS:

; LENGTH: 1997 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-750-134A-6  
  
Query Match 12.7%; Score 234.6; DB 2; Length 1997;  
Best Local Similarity 55.5%; Pred. No. 4.4e-59;  
Matches 585; Conservative 5; Mismatches 429; Indels 36; Gaps 6;  
  
QY 55 TTTTCCAGATGAGAGCAAAAGTCACTCGGATCCAGAGCATGAATATATGCGACCACTTA 114  
Db 135 TGTTCCGATACGACACGCGCGCATCGTGTCTATCCGACCGCTAAAGTGGGCTCATGA 194  
QY 115 AGTGTCTTCCACGTGATCATCTTTTCCCTACG---TTTGTCTTTCTGCTGGTAGTACA 171  
Db 195 ACCGCGGCTGCAGCTGCTCATCTGCTTACGTCATCGGCTGGGTGGTGTCTGTTGGGAAA 254  
QY 172 AGCTGTACAGCGGAAAGAGCCTGTCTATCAGTCTGTGCACACCAAGGTGAAGGGATAG 231  
Db 255 AGGGCTACCAAGAAACGGACTCCGTGGTCTAGCTCGGTGACACCAACCAAGGCTGTGG 314  
QY 232 CAGAGGTGAAAGAGGAGATCGTGGAGATGGAGTGAAGAAGTTGTCGACAGTCTCTTTG 291  
Db 315 CTGTGACCAAC-----ACCTCTCAGCTTGGATTCGGGATCTGGACGCTGGGACATG 368  
QY 292 ACACCGCAGATACACCTTCCCTTTGAGGGGAACTTTTCTTCTGTGATACAAACTTTC 351  
Db 369 TGATTCAG-----CTCAGGAGGAAACTCCCTCTTATTATGACCAACATGA 416  
QY 352 TCAAAACAGAGGCCAAGAGCAGCGGTTGTGCCGAGTATCCACCGCAGGACGCTCT 411  
Db 417 TTGTCACTGACACAGACACAGAGACCTGTCCAGAGATCTCTGATAAGACCAAGCATTT 476  
QY 412 GTTCTCTGACGAGGTTGTAAAGGATGGATGACCCGACAGAGCAAGAGATTCAGA 471  
Db 477 GTAATTCAGCGCGACTGCTCTCTGCTCCGTCAGACACCCAGGAGGAGTGGAGTCGGA 536  
QY 472 CCGGAGGTGTGTAGTATYATGAAGGGAACCAAGAGACCTGTGAAGTCTCTCTCTGTTGCC 531  
Db 537 CTGGAAGATGTGTCTCTTCAATGAGTCTGTGAAGACTGTGAGGTGCTCATGTTGCC 596  
QY 532 CCATTCAGGAGTGAAGAGCGCCCCCGGCTCTCTTTGAACAGTCCCGAAACTTCA 591  
Db 597 CGGTGAGAACGACGTTGGCGTGGCAACCGCGGCTTCTTAAAGGCTGCAGAAACTTCA 656  
QY 592 CTGTGCTCATCAGAACAAATATCGACTTCCCGGCCACACTACACACAGAGAAATCC 651  
Db 657 CCTCTTGGTAAGAACAAATCTGTTACCCCAAGTTTAACTTACGAGGAGAACATCC 716  
QY 652 TGGCAGGTTTAA-----ACATCACTTGTATCTTCCACTTCCACAAGACTCA---GAATCCAC 699  
Db 717 TCCCAACATCACCAGCTCTACTCAATCTGCAATTTACATCTCTCAACGGATCCCT 776  
QY 700 AGTGTCCCATTTCCGACTAGAGACATCTCCGAGAAACAGCGGATAAATTTTCAGATG 759  
Db 777 TCTGCCCATATTTCCGTCTTGGCAAACTCGTGGGAGCCGCGGACATAGCTTCCAGSAGA 836  
QY 760 KSGCAATTGAGGGCGGAATATGCGCAATTCAGATCTACTGGGACTGCAACTAGACCGTT 819  
Db 837 TGGCAGTTGAGGGAGGCAATCATGGGTATCCAGATCAAGTGGGACTGCAACTGGATAGAG 896  
QY 820 GGTTCATCACTGCGCTCCCAATACAGTTTCCCTCGCTTGAACAGACACCAACG 879  
Db 897 CGGCTCCCTTGTGCTGCCAGATATTCCTTCCGCGCGCTGGACACCCCGGACCTGGAAC 956  
QY 880 TGTCTTGTACCTGGCTACAACTTCAGATACGCCAAGTACTTACAGGA---AAACAATG 936  
Db 957 ACAATGTGCTCTCTGCTTACATTTTCAGTTTCCCAAGTACTTACAGGACCTGCCCGCA 1016  
QY 937 TTGAGAAACGGACTCTGATAAAGTCTTCCGGATCCGTTTGTACATCTGTTTGGCA 996

Db 1017 AAGAGCAGCGACACTCACCAGGCGTAGCGATCCGCTTGACATCATCGTGTGGAA 1076  
Qy 997 CCGGAGGAAATTTGACATATCCAGCTGGTGTGTGATCGGCTCAACCCCTCTACT 1056  
Db 1077 AGGCTGGGAGATTTGACATATCCCTTACCATGATCAACGTTGGCTTGGCTGGCGTCC 1136  
Qy 1057 TCGGCTGGCGCTGTGTTATCGAGCTTCCCTCATC 1091  
Db 1137 TCGGGGTGGCGAGCGTCTGTGAGCTCATAGTC 1171

## RESULT 6

US-09-363-745-6  
; Sequence 6, Application US/09363745  
; Patent No. 6194162  
; GENERAL INFORMATION:  
; APPLICANT: VALERA, SOLEDAD  
; APPLICANT: BUELL, GARY  
; TITLE OF INVENTION: P2X RECEPTORS (PURINOCEPTOR FAMILY)  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/363,745  
; FILING DATE:

; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/750,134  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CRAWFORD, ARTHUR C.  
; REGISTRATION NUMBER: 25,327  
; REFERENCE/DOCKET NUMBER: 1430-116  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 816-4006  
; TELEFAX: (703) 816-4100  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1997 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-09-363-745-6

Query Match 12.7%; Score 234.6; DB 4; Length 1997;  
Best Local Similarity 55.5%; Pred. No. 4.4e-59;  
Matches 585; Conservative 5; Mismatches 429; Indels 36; Gaps 6;

Qy 55 TTTTCAGTATGAGACGACAAAGTCACTCGGATCCAGACATGAATATGACCAATTA 114  
Db 135 TGTTCAGTATGAGACGACGCGGATCGTCTCATCCGAGCGGTAAAGTGGGGCTCATGA 194  
Qy 115 AGTGGTTCTCCACATGATCTTTTCTCTAG--TTTGTCTTCTCTGTTGAGTGACA 171  
Db 195 ACCGCGGCTGAGCTGCTCATCTGCTTACGTCATCGGTGGGTGTTCTGTTGGGAAA 254  
Qy 172 AGCTTACGAGCGGAAAGCGCTGTCATCATCTTGTGCACACCAAGGTGAAGGGGATAG 231  
Db 255 AGGGCTACCGAGGAAGCGACTCCGTTGTGTCAGCTCGTGCACACCAAGCAAGGTGG 314  
Qy 232 CAGAGTGAAGAGAGATCGYGAGATGGAGATGGAGTGGTGGTCACATGCTCTTG 291

Db 315 CTGTGACCAAC-----ACCTCTCAGCTTGGATTCGGATCTGGGACGTGCGGACTATG 368  
Qy 292 ACACCGGAGACTACACCTTCCCTTGGAGGGAACATCTCTTCTGATGATGACAAACTTTC 351  
Db 369 TGATTCAG-----CTCAGGAGGAAACTCCCTCTTCATTATGACCAACATGA 416  
Qy 352 TCAAAACAGAAAGCCCAAGAGCAGGGTGTGTCCTCCAGTATCCACCGGACGAGCTCT 411  
Db 417 TTGTACCCGTGAACACAGACAGACACCTGTCCAGAGATCTCTATAGACCAAGATTT 476  
Qy 412 GTTCTCTGACCGAGGTGTGTAAGAGGATGATGAGACCGCAGAGCAAGAAATTCAGA 471  
Db 477 GTAATTCAGACGCGGACTGCACTCTGCTCGGTGACACCCACAGCAGTGGCTTCGA 536  
Qy 472 CCGGAAGGTGTGATGATGATGAGGAAACAGAGACCTGTGAAGTCTCTGCTCTGCTG 531  
Db 537 CTGGAAGATGTGTTCTTCAATGAGTCTGTGAGAGCTGTGAGTGGCTCATGTTGGTCC 596  
Qy 532 CCATCGAGGAGTGGGAAGAGGCCCCCGGCTGCTCTTGAACAGTCCGAAACATTC 591  
Db 597 CGTGGGAAGACGAGCTGGCTGCGCAACGCGGCTTCTTAAAGCTCGAGAAACTTCA 656  
Qy 592 CTGTCTCATCAAGAAATATCGACTTCCCGGCCACAACTACACACAGAGAAACATCC 651  
Db 657 CCTCTTGGTAAAGAAACAATCTGGTACCCCAAGTTTAACTTCAGCAAGAGAAACATCC 716  
Qy 652 TCCAGAGTTTAA-----ACATCACTTGTACCTTCCACAGACTCA---GAATCCAC 699  
Db 717 TCCCCAATCATCACACGCTCTTACCTCAATGCTGATTTACATGCTCAACGATCCCT 776  
Qy 700 AGTGTCCATTTTCCGACTAGGAGACATCTTCCGAGAAACAGCGCATATTTTTCAGATG 759  
Db 777 TCTGCCCATATTCCTGCTTGGCAATCTGGGGGACGCGGACATAGCTTCCAGGAGA 836  
Qy 760 KGCATTTACGGGGGAATAATGAGCATGATGATCTACTGAGTCTGCAACCTAGACCTT 819  
Db 837 TGGCAGTTGAGGGAGCATCATGAGTATCCAGATCAAGTGGGACTGCAACCTGGATAG 896  
Qy 820 GGTTCATCACTGCTCCCAATACAGTTTCCCTGCGCTTGCAGCAGACAGACCAACG 879  
Db 897 CGCTCTCCCTTGGCTGCGCAATATTTCTTCCGCGCTTGCAGACCCCGGACCTGGAC 956  
Qy 880 TGTCTTGTACCTTGGCTACAACTTACAGATGACGCAAGTACTACAAGGA---AAACAATG 936  
Db 957 ACAATGTCTCTCTGCTACAACTTTCAGTTTGGCAAGTACTACAGGAGCACTGCGGCA 1016  
Qy 937 TTGAGAAACGAGCTCTGATAAAGTCTTCGGGATCCGTTTGTACATCTCTGTTTGGCA 996  
Db 1017 AAGACGCGCACACTCCACAAAGCGGTACGGCATCCGCTTGTGACATCATGCTGTTG 1076  
Qy 997 CCGGAGGAAATTTGACATATCCAGCTGGTGTGTGTATCATCGCTCAACCTCTCTACT 1056  
Db 1077 AGGCTGGGAGTTTGACATCATCCCTACCATGATCAAGTTGGCTCTGCTGGCGCTCC 1136  
Qy 1057 TCGGTCTGGCCRCGTGTGTTCATCGAGCTTCTCTCATC 1091  
Db 1137 TCGGGGTGGCAGCGTCTCTGTGAGCTCATAGTC 1171

## RESULT 7

US-08-750-134A-10  
; Sequence 10, Application US/08750134A  
; Patent No. 5985603  
; GENERAL INFORMATION:  
; APPLICANT: VALERA, SOLEDAD  
; APPLICANT: BUELL, GARY  
; TITLE OF INVENTION: P2X RECEPTORS (PURINOCEPTOR FAMILY)  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA

```

1033 A-----ATCTCTCCCGAGGCTTCAACTTACAGTTTGCAGGCACTTTGTGGAGAAC 1073
QY 933 AATGTTGAGAAACGGACACTCTGATAAAAGTCTTCGGGATCCGTTTGTACATCTCGTGT 992
Db 1074 GGGACCAACTACCGTCACTCTTCAAGGTGTTGGATTCGCTTTGACATCTCGTGGAC 1133
QY 993 GGCACGGGAGGAAAATTGTGACATTTATCCAGCTGGTGTGTATCATCGGCTCAACCCCTCC 1052
Db 1134 GGCAAGCGCGGAAGTTTGGACATCATCCCTACAATGACACCATCGCTCTGGAATTGGC 1193
QY 1053 TACTTCGGTCTGGCCRCCTGTGTTCATCGACTTCCT 1087
Db 1194 ATCTTGGGTGGCCACAGTTCTCTGTGACCTGCT 1228

RESULT 8
US-09-363-745-10
; Sequence 10, Application US/09363745
; Patent No. 6194162
; GENERAL INFORMATION:
; APPLICANT: VALERA, SOLEDAD
; APPLICANT: BUELL, GARY
; TITLE OF INVENTION: P2x RECEPTORS (PURINOCEPTOR FAMILY)
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/363,745
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/750,134
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAWFORD, ARTHUR C.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 1430-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4006
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2643 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-363-745-10

Query Match 11.0%; Score 203.8; DB 4; Length 2643;
Best Local Similarity 54.8%; Pred. No. 6.5e-50;
Matches 447; Conservative 5; Mismatches 342; Indels 21; Gaps 2;

QY 285 GTCTTTGACACGGCAGACTACACTTCCCTTCCTCCAGGGGAACCTCTTCTTCGTGATGACA 344
Db 423 GTCTGGGATGTGGCTGACTGCTCTCCAGCCAGGGGGAACAACCTCTTCGTGGTCTATG 482
QY 345 AACCTTTCTCAAACAGAGAGGCAAGACAGCGGTTGTGTCCCGAGTATCCACCCGAGG 404
Db 483 ACCAATTTTCACTCGTGACCCCGAAGCAGACTCAGGCTACTCGGAGAGACCCAGAGGG 542
QY 405 ACGTCTGTGTTCTCTGACCTGAGGTTGTAAAGAGGATGGATGGACCGCAGACAAAGGA 464

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543	Db	GGCATATGCAAGGAAGACAGTGGCGCTGTGACCCCTGGGAAGGCCAACAGAGAGGCCCAAGGC	602
465	QY	ATTACGACCCGGAAGTGTGTAGTATGAAAGGAACACAGAAGACCTGTGAAGTCTCTGCC	524
603	Db	ATCGCACGGCAAGTGTGGCCTTCAAGCACACTGTGAGACGCTGTGAGATCTTTGGC	662
525	QY	TGTTGCCCATCGAGGAGTGGGAAGAGGCCGCCGCCCTGCTCTCTTGAAACAGTGGCGAA	584
663	Db	TGTTGCCCGCTGGAGGTGGATGAGCAGCATCCGCGGCCCTGCCCTTCTCGAGAGGCCGAG	722
585	QY	AACCTTCACTGTGCTCATCAAGAAACAATATGCACTTCCCGGCCACAACTACACACAGAGA	644
723	Db	AACCTTCACTCTTTTCATCAAGACAGCATCAGCTTTCACGCTTCAGAGTCACAGGGCGC	782
645	QY	AACATCCTGGCAGTTTTAAA-----CATCACTTGTACCTTCCACAGACTCAG	692
783	Db	AACCTGGTGGAGGAGTGAATGCTGCCCATGAAGACCTGCCTCTTTTCACAAAGACCCGTG	842
693	QY	AATCCACAGTGTCCATTTTCCGACTAGAGACATCTTCGAGAAACAGCGCATATTTT	752
843	Db	CACCCCTGTGCCAGTCTTCCAGCTTGGCTACGTGTGCAAGAGTCGCGCCGAGAACTTC	902
753	QY	TCAGATGKGGAATTCAGGGCGGAATAAATGGGCAATGAGATCTACTGGGAGTCAACCTA	812
903	Db	AGCACCCCTGGCTGAGAAGGGTGGAGTGGTGGCATCACATCGACTGGCATGTGACCTG	962
813	QY	GACCGTGGTTCATCATCTGCTGCCATCCCAATACAGTTTCCTCGCCTTGACACACAGACC	872
963	Db	GATGGCAGTACGGCATCGAGACCCCATCTATGAGTTTCCATGGCTACGAGAGAAA	1022
873	QY	ACCAAGTGTCTTGTACCTCGGCTCAACTTCAGATACGCCAAGTACTACAGAGAAAAC	932
1023	Db	A-----ATCTCTCCCCAGGCTTCAACTTCAGSTTTGCCAGGCACTTTGTGGAGAAC	1073
933	QY	AATGTTGAGAAACGACATCTGATAAAGCTTTCGGGATCCGTTTTTGACATCCCTGGTTTT	992
1074	Db	GGACCAACTCCGTCACCTCTTCAAGGTGTTGGGATTCGCTTTTGACATCCCTGGTGAC	1133
993	QY	GGCAGCGGAGGAAAAATTGACATATATCCAGCTGGTGTGTACATCGGCTCAACCCCTCC	1052
1134	Db	GGCAAGGCCGGGAAGTTTGATCATATCCCTACAATGACCCACCTCGGCTTGGATTTGGC	1193
1053	QY	TACTTCGGTCTGGCGRCTGTGTTCAAGGACTTCCT	1087
1194	Db	ATCTTTGGGGTGGCCACAGTCTCTGTGTGACCTGCT	1228

## RESULT 9

US-08-750-134A-4  
; Sequence 4, Application US/08750134A  
; Patent No. 5985603

GENERAL INFORMATION:

APPLICANT: VALERA, SOLEDAD

APPLICANT: BUELL, GARY

; TITLE OF INVENTION: P2X RE

; NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON &amp; VANDERHYE ;

STREET: 1100 NORTH GLEBE

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: U.S.A.

; ZIP: 22201-4714

; COMPUTER READABLE FORM:

```

;
; MEDIUM TYPE: Floppy disk

```

COMPUTER: IBM PC compatible

```

; OPERATING SYSTEM: PC-DOS,
;

```

```

; SOFTWARE: PatentIn Release
; CURRENT ADDITION NUMBER:

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;; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/0
: FILING DATE: 22-JAN-1997

```

FILING DATE: 22-JAN-1997  
CLASSIFICATION: 536

CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:





```

; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,134A
; FILING DATE: 22-JAN-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAWFORD, ARTHUR C.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 1430-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4006
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1753 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-750-134A-8

```

Query Match 7.6%; Score 140.2; DB 2; Length 1753;

Best Local Similarity 52.6%; Pred. No. 3e-31;

Matches 457; Conservative 3; Mismatches 376; Indels 33; Gaps 6;

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QY 254 GGAGATGAGTGAAGAGTGGTGACAGTGTCTTGACACCCGACACTACACCTTCC 313
DB 351 GGTGAAGAGTCCGGGCGCTATGCCACAGAGTATGACGTGTCGGATTATGTACCCC 410
QY 314 TTTCAGGGGAACTCTTTCT--TCGTGATGACAACTTCTCAAAACAGAGGCCAAGA 370
DB 411 ACCCAGGCGACCTCTGTCTTGTGTCATCATCAACCAATGATCGTTACTGAAATCAAT 470
QY 371 GCAGCGTGTGTCGCGAGTATCCACCCGAGGAGCTCTGTCCTCTGACCGAGGTG 430
DB 471 GCAAGGATTTCTTCCAGAGAT---GAAGAGAGTACCCGCTGTGTCTGACAGCCAGT 527
QY 431 TAAAGAGGATGGATGGACCGGACGAAAGGAATTCAGACCCGGAAGGTGTGTATGTA 490
DB 528 TGGCCCTGAACG-----CTTCCAGGTGGGGGATCTCACCAGCGCGCTGCGTGACATA 581
QY 491 TGAAGGAACACAGAGACTGTGAAGTCTCTGCTGGTGGTCCCATCGAGGCACTGGAAGA 550
DB 582 CAGCTGTCTTCTCCGAGACTGTGAGATCCAGGCGTGGTGGCCCA-----CTGAGGTGA 635
QY 551 GCGCCCGCGGCTGTCTCTTGACAGTGCAGGAACTTCACTGTCTCATCAAGAAACA 610
DB 636 CACCGTGGAGATGCCCTATCATGATGGAGGCTGAGACTTCACCAITTTTCATCAAGAAC 695
QY 611 TATCGACTTCCCGGCAACATACACACGAGAAATCTCTCCAGGTTTAAACATCAC 670
DB 696 CATCCGTTCCCTCTCTCACTTTGAGAGGGAACCTCTGCGCTAACCTACCGAACAA 755
QY 671 T-----TGTAACCTCCACAAGACTCAGAAATCCACAGTGTCCCATTTTCGAGCT 718
DB 756 GGACATAAAGAGGTGCCGCTTCCACCCCTGAAAGGGCCCATTTTGGCCCATCTTGAGGT 815
QY 719 AGGAGACATCTCCAGAAACAGCGGATATATTTTTCAGATGKGGCAATTCAGGCGGAA 778
DB 816 AGGGGATGTGGTATAGTTTGTGGACAGAGATTTTGCAAGCTGGCCGCGCAGGCGGT 875
QY 779 AATGGGATGAGATCTACTGGACTGCAACCTAGACCGTGGTTCATCACTGCGCTCC 838

```

# RESULT 14

US-09-363-745-8

; Sequence 8, Application US/09363745

; Patent No. 6194162

; GENERAL INFORMATION:

; APPLICANT: BUELL, GARY

; APPLICANT: VALERA, SOLEDAD

; TITLE OF INVENTION: P2X RECEPTORS (PURINOCEPTOR FAMILY)

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: U.S.A.

; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/363,745

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/750,134

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: CRAWFORD, ARTHUR C.

; REGISTRATION NUMBER: 25,327

; REFERENCE/DOCKET NUMBER: 1430-116

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 816-4006

; TELEFAX: (703) 816-4100

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1753 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cdna

US-09-363-745-8

Query Match

Best Local Similarity 7.6%; Score 140.2; DB 4; Length 1753;

Matches 457; Conservative 3; Mismatches 376; Indels 33; Gaps 6;

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QY 254 GGAGATGAGTGAAGAGTGGTGACAGTGTCTTGACACCCGACACTACACCTTCC 313

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181 AGCGAAGAGAGCTGTTCATCAGTTCGTGTCACACCAAGGTGAAGGGGATAGCAGAGGTGA 240  
181 AGCGAAGAGAGCTGTTCATCAGTTCGTGTCACACCAAGGTGAAGGGGATAGCAGAGGTGA 240  
241 AAGAGAGATCGYGAGATGAGAGTGAAGAGTGGTGACAGTGTCTTTGACACCCGAG 300  
241 AAGAGAGATCGYGAGATGAGAGTGAAGAGTGGTGACAGTGTCTTTGACACCCGAG 300  
301 ACTACACCTCCCTTCAGGGGAACTCTTCTCGATGACAAACTTCTCAAAACAG 360  
301 ACTACACCTCCCTTCAGGGGAACTCTTCTCGATGACAAACTTCTCAAAACAG 360  
361 AAGGCAAGAGACAGCGTGTGTCCCGAGTATCCACCCGAGAGCGTCTCTTCCCTG 420  
361 AAGGCAAGAGACAGCGTGTGTCCCGAGTATCCACCCGAGAGCGTCTCTTCCCTG 420  
421 ACCGAGGTGTAAAGAGGATGATGGAGCCGACAGCAAGAAATCAGACCGGAGGT 480  
421 ACCGAGGTGTAAAGAGGATGATGGAGCCGACAGCAAGAAATCAGACCGGAGGT 480  
481 GTGTAGTATGAAAGGAACAGAGACCTGTGAAGTCTGTGCTGTGCTGCCCATCGAGG 540  
481 GTGTAGTATGAAAGGAACAGAGACCTGTGAAGTCTGTGCTGTGCTGCCCATCGAGG 540  
541 CAGTGGAAAGAGGCCCCCGGCTGTCTTTGAACAGTGGCGGAACTTCACTGTGCTCA 600  
541 CAGTGGAAAGAGGCCCCCGGCTGTCTTTGAACAGTGGCGGAACTTCACTGTGCTCA 600  
601 TCAAGAACAAATGACATCTCCCGGACACACTACACCAAGAGAACTCTTCCGAGGT 660  
601 TCAAGAACAAATGACATCTCCCGGACACACTACACCAAGAGAACTCTTCCGAGGT 660  
661 TAAACATCACTGTACCTTCCACAGACACAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 720  
661 TAAACATCACTGTACCTTCCACAGACACAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 720  
721 GAGACATCTCCGAGAAACAGGCGATAATTTTCAGTGGGCAATTCAGGCGGAAATPAA 780  
721 GAGACATCTCCGAGAAACAGGCGATAATTTTCAGTGGGCAATTCAGGCGGAAATPAA 780  
781 TGGGATTCAGATCTACTGGGACTGCAACCTAGACAGTGTGCTTCCATCACTGCTTCCCA 840  
781 TGGGATTCAGATCTACTGGGACTGCAACCTAGACAGTGTGCTTCCATCACTGCTTCCCA 840  
841 AATACAGTTTCCTCGCTTTCAGACACAGACACCAAGCTGCTGCTGCTGCTGCTGCTGCT 900  
841 AATACAGTTTCCTCGCTTTCAGACACAGACACCAAGCTGCTGCTGCTGCTGCTGCTGCT 900  
901 ACTCAGATACCGCAAGTACTACAGAAACAAATGTTGAGAACGAGTCTGTGAATAAG 960  
901 ACTCAGATACCGCAAGTACTACAGAAACAAATGTTGAGAACGAGTCTGTGAATAAG 960  
961 TCTTGGGATCCGTTTACATCTCTGTTTGGACCGGAGGAAATTTGACATATCC 1020  
961 TCTTGGGATCCGTTTACATCTCTGTTTGGACCGGAGGAAATTTGACATATCC 1020  
1021 AGCTGGTGTGTACATCGCTCAACCTCTCTACTTGGCTGCGCTGCTGCTGCTGCTGCTGCT 1080  
1021 AGCTGGTGTGTACATCGCTCAACCTCTCTACTTGGCTGCGCTGCTGCTGCTGCTGCTGCT 1080  
1081 ACTTCTCATGACASTTACTCCAGTAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
1081 ACTTCTCATGACASTTACTCCAGTAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
1141 AGTGTGTGTACGCTGTGTGTCAGCAATCTACTACAGAGAGAGTGGAGTCCATG 1200  
1141 AGTGTGTGTACGCTGTGTGTCAGCAATCTACTACAGAGAGAGTGGAGTCCATG 1200  
1201 TGGAGCCAAAGCCGACATTAAGTATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260  
1201 TGGAGCCAAAGCCGACATTAAGTATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260

1261 TGAACACAGCAGCTACTAGGAGAGAGTGTCAAGATGTCAAGGGCCCAAGAGTCCSAAGAC 1320  
1261 TGAACACAGCAGCTACTAGGAGAGAGTGTCAAGATGTCAAGGGCCCAAGAGTCCSAAGAC 1320  
1321 CTGTGATGGATCTTCAAGATTTGTCCAGGCTGCCCCCTGCGCCCTCCATGACACACCCCCGA 1380  
1321 CTGTGATGGATCTTCAAGATTTGTCCAGGCTGCCCCCTGCGCCCTCCATGACACACCCCCGA 1380  
1381 TTCTTGGACACACAGAGAGATACGCTGTAGAAAGAGGAGGAGCTCTAGATCCAGGG 1440  
1381 TTCTTGGACACACAGAGAGATACGCTGTAGAAAGAGGAGGAGCTCTAGATCCAGGG 1440  
1441 ATAGCCCTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500  
1441 ATAGCCCTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500  
1501 GTGTGCTGAGGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560  
1501 GTGTGCTGAGGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560  
1561 TGTTCAGGAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620  
1561 TGTTCAGGAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620  
1621 CTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680  
1621 CTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680  
1681 GCTAGCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740  
1681 GCTAGCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740  
1741 GCT 1800  
1741 GCT 1800  
1801 AGAGTCTTACTGAAGCAGGACCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1853  
1801 AGAGTCTTACTGAAGCAGGACCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1853

## RESULT 2

US-10-175-523-191  
; Sequence 191, Application US/10175523  
; Publication No. US20030096264A1  
; GENERAL INFORMATION:  
; APPLICANT: Brockman, Jeffrey  
; APPLICANT: Evans, David  
; APPLICANT: Hook, Derek  
; APPLICANT: Klimczak, Leszek  
; APPLICANT: Laeng, Pascal  
; APPLICANT: Palfreyman, Michael  
; APPLICANT: Rajan, Prithi  
; TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)  
; FILE REFERENCE: 3235/J795-US3  
; CURRENT APPLICATION NUMBER: US/10/175,523  
; PRIOR FILING DATE: 2002-06-18  
; PRIOR APPLICATION NUMBER: US 60/299,151  
; PRIOR FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: US 60/317,828  
; PRIOR FILING DATE: 2001-09-07  
; PRIOR APPLICATION NUMBER: US 60/325,150  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US 60/333,047  
; PRIOR FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: US 60/349,936  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: US 60/361,834  
; PRIOR FILING DATE: 2002-03-04  
; NUMBER OF SEQ ID NOS: 197  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 191  
; LENGTH: 2164

RESULT 3  
US-09-833-082-1  
; Sequence 1, Application US/09833082  
; Patent No. us20090151480v1

```

1  APPLICATION: CHRM, MYOUNG
2  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
3  TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 10218
4  FILE REFERENCE: MNI-227
5  CURRENT APPLICATION NUMBER: US/09/833,082
6  CURRENT FILING DATE: 2001-04-10
7  NUMBER OF SEQ ID NOS: 2
8  SOFTWARE: FastSeq for Windows Version 4.0
9

```

```
; SEQ ID NO 1
; LENGTH: 1389
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-833-082-1

Query Match      12.8%; Score 237; DB 11; Length 1389;
Best Local Similarity 54.4%; Pred. No. 3,9e-64;
Matches 574; Conservative 5; Mismatches 440; Indels 35; Gaps 4;

QY 55 TTTTCAGTATGAGACGACAAAGTCACCTCGGATCCAGAGCATGAATATGACACCATTA 114
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 62 TTTTCAGTATGAGACGACGCGCATCGTCATCCGAGCGCGAAGTGGGCTCATGA 121
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 115 AGTGGTTCTCCAGTGATCATCTTTTCTAG---TTGCTTTGCTCTGGTGAAGTGACA 171
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 122 ACGGCGCGTCACTGCTCATCTGGCTAGCTCATCGGTGGTGGTGGTGGGAAA 181
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 172 AGCTGTACACGCGGAAGACCTGTCTCATCAGTGTCTGTGCACCAAGGTGAAGGGATAG 231
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 182 AGGGCTTACAGGAAACTGACTCCGTGTCTAGCTCGGTTCAGCAAGGTCAAGGGCGTGG 241
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 232 CAGAGGTGAAGAGAGATCGYGGAAGTGGAGTGAAGTGGTGGTGCACAGTCTTTG 291
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 242 CTGTGAACCAACTTCTAACTTGGATTCCGGATCTGGGATGGGGAATTATGTGATAC 301
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 292 ACACGCGACATACACCTTCCTTTGCAGGGAAGTCTTTCTTGTGATGACAAACTTTC 351
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 302 CAG-----CTCAGAGAGAAACTCCCTCTCTGCTCATGACCAACGTGA 343
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 352 TCAAAACAGAGGCGCAAGAGCAGCGGTGTGTCCGAGTATCCACCCGAGAGAGCTCT 411
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 344 TCCTCACCATGAACAGACACAGCGGCTGTGCCCGAGATTCCAGATGGGACCACTGTGT 403
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 412 GTTCTCTGACCGAGTTGTAAAGAGTGGATGGACCCGACAGCAAGGAATTCAGA 471
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 404 GTAAATCAGATGCCAGTGTACTGCCGGCTGTGCCGGCACCCACAGCAAGGCTCTCAA 463
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 472 CCGGAAGGTGTAGTATATGAAGGAACAGAGACCTGTGAAGTCTGTGCTGTGCTGCC 531
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 464 CAGGAGGTGTGCTAGCTTTCAAGGGTTCGTCAAGACGTGTGAGTGGGGCTGTGCTGCC 523
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 532 CCATGCGAGCTAGTGAAGAGGCCCCCGGCTGTCTCTTGAACAGTGGCGAAAACCTTCA 591
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 524 CGGTGGAGATGACACACAGTGCACAACTGTCTTTTAAAGGCTGCAGAAAACCTTCA 583
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 592 CTGTGCTCATCAGAACAAATATCGACTTCCCGGGCCCACTACACCCAGCAAGAACATCC 651
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 584 CTCCTTTGGTTAAGAACAAATCTGGTATCCCAAAATTTAATTTCAGCAAGAGGAATATCC 643
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 652 TGGCAGGTTTAAACATCACT-----TGTACCTTCCACAGACTCAGAAATCCAC 699
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 644 TTCCCAACATCACCACACTACTTACCTCAAGTGTGATTTATGATGAACAGATCCCT 703
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 700 AGTGTCCCAATTTCCGACTAGAGACATTTCCGAGAAACAGCGGATTAATTTTCAGATG 759
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 704 TCTGCCCATATTTCCGTCTTGGCAAAATAGTGGAGAACGACGAGACAGTTTCCAGGACA 763
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 760 KGCATATCAGGGGGAATATGGCATTGAGATCTCTGAGTGCACACCTAGACCGT 819
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 764 TGGCCGTGGAGGAGGATCATGGGATCCAGGTCACTGGGACTGCACCTGGACAGAG 823
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 820 GGTTCATCATCTGTCCTCCAAATACAGTTTTCCTTCGCTTGTGACGACAGACCAACAG 879
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 824 CCGCCCTCTGTCTTCCAGGTACTCTTCCGGCGGCTCGATACAGGGAGCTGTGAGC 883
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 880 TGTCTTGTACCTGGGTACAACTTCAGATACGCCAAGTACTACAGGAAAACAATG--- 936
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 884 ACAACGTATCTCTGGGTACAATTTCAAGGTTTGGCAAGTACTACAGAGACTGGCTGSCA 943
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 937 TTGAGAAACGAGCTCTGATAAAGTCTTCGGATCCGTTTTCAGATCCGTTTTCGCA 996
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 944 ACAGAGCGGACAGCTCATCAAGSCCTATGGCATCCGCTTCGACATCATTTGTGTTGGGA 1003
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY 997 CCGGAGGAAAATTTGACATATATCCAGCTGGTTGTGTACATCGGCTCAACCTCTCTCTACT 1056
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1004 AGGAGGAAAATTTGACATATATCCAGCTGGTTGTGTACATCAACATCGGCTCTGGCTGGCACTGC 1063
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1057 TCGGCTGTGCGCTGTGTTCATCGACTTCTCTCATC 1091
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1064 TAGGCATGGCAGCGTCTGTGTGACATCATAGTC 1098
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RESULT 4
US-09-969-347-225
; Sequence 225, Application US/09969347
; Patent No. US20020115085A1
; GENERAL INFORMATION:
; APPLICANT: Emner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Si;
; FILE REFERENCE: Sets
; CURRENT APPLICATION NUMBER: US/09/969,347
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/60/237,598
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US/60/237,604
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 318
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 225
; LENGTH: 2633
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-969-347-225
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Query Match      11.08; Score 203.8; DB 11; Length 2633;
Best Local Similarity 54.8%; Pred. No. 2e-53;
Matches 447; Conservative 5; Mismatches 342; Indels 21; Gaps 2;
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QY 285 GTCTTTGACACGACAGACTACCTTCCCTTTTCAGGGGAACCTCTTCTTCGTGATGACA 344
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 446 GTCTGGATGTGGCTGACTAGCTCTTCCAGCCAGGGGAGCACTCTTCTGTGTGCTATG 505
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 345 AACTTCTTCAAAACAGAGGCCAAGAGCAGCGGTTGTCTCCGAGTATCCACCCGCGAGG 404
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 506 ACCAATTTTCATCGTGACCCGCAAGAGCAGACTCAAGGCTACTGCCGAGACACCCAGAGGG 565
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 405 AGCTCTGTCTCTGACCGAGGTTCTTAAAGAGATGGATGAGCCCGCAGAGCAAGAGA 464
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 566 GGCATATGCAAGAGAGACAGTGGCTGTACCCCTGGGAAGGCCAAGAGAGGCCCAAGGC 625
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 465 ATTCAGACCGGAAGGTGTGTAGTATGAAGGGAACACAGAGACCTGTGAACTCTCTGCC 524
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Db 626 ATCCGACGCGCAAGTGTGTGGCTTCAACGACACTGTGAGAGGCTGTGAGATCTTTGGC 685
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 525 TGGTGCCCATCGAGAGCAGTGGAGAGGCCGCCCGGCTGTCTCTTTGACAGTGGCCGAA 584
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 686 TGGTGCCCGGTGGAGTGGATGACGACATCCGCGGCTGTGCCCTTCTCCGAGAGCCGAG 745
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 585 AACTTCACCTGTCTCATCAAGAACAAATATCGACTTCCCGGCCACAACTACACACAGAGA 644
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 746 AACTTCACCTTCTTTTCAAGAACACATCAGCTTTCCACGCTTCAAGTCAACAGGCGC 805
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 645 ACATCTCTGCCAGGTTTAAA-----CACTACTTGTACCTTCCCAAGACTCAG 692
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 806 ARCTTGTGGAGAGGTGATGTGCCACATGAGACCTGCCTCTTTCACAGACCTTG 865
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 693 AATCCACAGTGTCCCATTTTCGACTTAGAGACATCTTCCGAGAAACAGGCGCAATTTT 752
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Db 866 CACCCCTCTGCCAGTCTTCCAGCTTGGCTAGCTGTGGTGAAGAGTCAGGCCAGAACTTC 925
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 753 TCAGATGGGCAANTCAGGCGCGAATAATGGSCATTTAGATCTACTGGGACTGCAACCTA 812
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 926 AGCACCTTGGTGAGAGAGGTGGAGTGTGGCATCCACCATGACACTGGCACTGTGACCTG 985
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[illegible]

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RESULT 14
US-09-998-598-1742
? Sequence 1742, Application US/09998598
? Patent No. US20020150922A1
? GENERAL INFORMATION:
? APPLICANT: Stolk, John A.
? APPLICANT: Xu, Jiangchun
? APPLICANT: Chenuault, Ruth A.
? APPLICANT: Meagher, Madeleine Joy
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
? TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
? FILE REFERENCE: 210121.561
? CURRENT APPLICATION NUMBER: US/09/998,598
? CURRENT FILING DATE: 2001-11-16
? NUMBER OF SEQ ID NOS: 2606
? SOFTWARE: Corlax Invention Disclosure Database
? SEQ ID NO 1742
? LENGTH: 229
? TYPE: DNA
? ORGANISM: Homo sapiens
US-09-998-598-1742

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Db      122 CATCATAGTC 131

RESULT 15
US-09-764-847-250
; Sequence 250, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 250
; LENGTH: 941
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: SITE
; LOCATION: (6)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (94)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (112)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (832)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (849)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (909)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-764-847-250

Query Match      2.8%; Score 51.2; DB 11; Length 941;
Best Local Similarity 54.3%; Pred. No. 3.le-05;
Matches 139; Conservative 4; Mismatches 107; Indels 6; Gaps 2

QY      398  CCGCAGGACGCTCTGTCTCTGTACCCGAGGTTGTAAGGAGGATGGATGGACCGCGAGAG 457
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DB      564  CCACAAGCCACCTGCTCTCCGAGCCGACTGCGTGGCTGGGAGCTGGACATGCTGGG 623

QY      458  CAAGAGAAATTCAGACCGGAGGTGTGTAGTAT---GAAGGGAACCAAGAGACCTGTGA 514
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      624  AAACGGCTGAGGACTGGGCGCTGTGTGCGCTATTACAGGGGGCCCTCCAAAGACCTGCGA 683

QY      515  AGTCTGCTGCTGTGCCCCATCGAGGCGATGGAAGAGGCCCCCGCGCTGTCTCTTGA 574
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      684  GGTGTTGCGTGTGCGCC---GGTGAAGATGGGGCCTCTGTACGCCAATTTCTGGGTAC 740

QY      575  CAGTGCAGAAATTCCTGCTGTCTCATCAAGAACAAATATCGACTTCCCGGCCCAACTA 634
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DB      741  GATGCCCCCAATTTCAACATTCATCAAGACACGATCTACCCCAATTCCTT 800

QY      635  CACCAGAGAACATC 650
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DB      801  CTCCAAGGGCAACATC 816
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```



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 18, 2003, 20:13:22 ; Search time 2709 Seconds  
(without alignments)  
11077.976 Million cell updates/sec

Title: US-09-977-221-2-C-AT-1513

Perfect score: 1853

Sequence: 1 aaacacgaggaggagct.....cgtctgtaatccacatttt 1853

Scoring table: IDENTITY\_NVC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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EST.*
1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estmd.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_htc.*
9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: gb_gss.*
18: em_gss_hum.*
19: em_gss_inv.*
20: em_gss_pln.*
21: em_gss_vrt.*
22: em_gss_fun.*
23: em_gss_mam.*
24: em_gss_mus.*
25: em_gss_other.*
26: em_gss_pro.*
27: em_gss_rod.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Match	Score	Length	DB	ID	Description
1	1635	88.2	3013	11	BC007679	Homo sapi
2	674	36.4	795	13	BI861622	603390486
3	671.8	36.3	946	12	BF347747	602022588
4	666.8	36.0	937	12	BG768165	602744202
5	645.4	34.8	932	13	BI603534	603244436
6	613.8	33.4	769	12	BG766449	602739207

7	564	30.4	860	13	BI598073
8	553.8	29.9	841	12	BG769595
9	547.4	29.5	908	12	BF689446
10	498.6	26.9	817	10	BE382829
11	486.4	26.2	1022	12	BF690388
12	430	23.2	543	12	BF347290
13	399.6	21.6	642	14	BQ554327
14	390.2	21.1	783	12	BG769470
15	373	20.1	555	12	BF347097
16	288.6	15.6	475	10	BE689531
17	246.2	13.3	247	9	AA210664
18	237	12.7	1844	11	BC017458
19	235.6	12.8	368	10	BE448796
20	225.2	12.2	1992	11	BC002099
21	211.8	11.4	910	14	BQ681359
22	210.2	11.3	937	13	BI687408
23	206.2	11.1	412	12	BF770342
24	201	10.8	867	14	BQ888542
25	200.6	10.8	844	9	AJ446359
26	191.6	10.3	659	10	AW913237
27	186.4	10.2	1051	9	AL544542
28	182.2	9.8	595	13	BI536809
29	181.8	9.8	244	9	AA672571
30	181.6	9.8	581	13	BI681932
31	181	9.8	331	10	AW899099
32	178.4	9.6	753	13	BI452907
33	178.4	9.6	847	9	AJ445426
34	168.2	9.1	261	12	BF928435
35	166.6	9.0	454	9	AI962024
36	161	8.7	276	9	AA362346
37	160.6	8.7	644	10	AW975596
38	156.2	8.4	1059	14	BM919221
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44	148.6	8.0	497	10	BE690562
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#### ALIGNMENTS

RESULT 1  
BC007679  
LOCUS  
DEFINITION  
Homo sapiens, Similar to purinergic receptor p2X, ligand-gated ion channel, 7, clone IMAGE:3628076, mRNA.  
ACCESSION  
BC007679  
VERSION  
BC007679.1  
KEYWORDS  
HTC.  
SOURCE  
Homo sapiens.  
ORGANISM  
Homo sapiens  
REFERENCE  
1 (bases 1 to 3013)  
Strausberg,R.  
Direct Submission  
Submitted (11-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
REMARK  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
COMMENT  
Contact: MGC help desk  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;  
Web site: <http://www.nisc.nih.gov/>





```

/note="Organ: brain; Vector: pCMV-SPORT6; Site1: NotI;
Site2: SalI; Cloned unidirectionally. Primer: Oligo dm.
Average insert size 2.3 Kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      237 a   254 c   251 g   204 t
ORIGIN
Query Match      36.38; Score 671.8; DB 12; Length 946;
Best Local Similarity 94.48; Pred. No. 3.1e-170;
Matches 758; Conservative 4; Mismatches 31; Indels 10; Gaps 6;
QY 5 CGCAGGGAGGAGGCTGTCCACCATGCCGCGCTCTGCGAGCTGCAGTGATGTTTCCAGTA 64
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Db 18 CGCAGGGAGGAGGCTGTCCACCATGCCGCGCTCTGCGAGCTGCAGTGATGTTTCCAGTA 77
QY 65 TGAGAGCAACAAGTCACTCGATGCCAGAGCATGAATATGGACCAATTAAGTGTCTT 124
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 78 TGAGAGCAACAAGTCACTCGATGCCAGAGCATGAATATGGACCAATTAAGTGTCTT 137
QY 125 CCACGTGATCATCTTTTCTACCTTTCTTCTGCTGAGTGACAGCTGTACCAGCG 184
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Db 138 CCACGTGATCATCTTTTCTACCTTTCTTCTGCTGAGTGACAGCTGTACCAGCG 197
QY 185 GAAGAGGCTGTATCATCTTTCTGTCACCAAGTGAAGGGGATAGCAGAGGTGAAGA 244
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Db 198 GAAGAGGCTGTATCATCTTTCTGTCACCAAGTGAAGGGGATAGCAGAGGTGAAGA 257
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Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 258 GGAGATCGTGGAGATGAGTGAAGAGTGTGTGACACAGTGTCTTTGACACCGCAGACTA 317
QY 305 CACCTTCCCTTTGACGGGAGACTCTTTCTGCTGATGACAAACTTTCTCAAAACAGAAGG 364
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 318 CACCTTCCCTTTGACGGGAGACTCTTTCTGCTGATGACAAACTTTCTCAAAACAGAAGG 377
QY 365 CCAAGAGCAGCGTTTGTGTCGAGTATCCACCGCAGAGCGTCTGTTCCTTCACCG 424
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Db 378 CCAAGAGCAGCGTTTGTGTCGAGTATCCACCGCAGAGCGTCTGTTCCTTCACCG 437
QY 425 AGCTTCTAAAGAGGATGGATGGACCGCAGAGCAAGGAATTCAGACCGGAGGTGT 484
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Db 438 AGTTTCTAAAGAGGATGGATGGACCGCAGAGCAAGGAATTCAGACCGGAGGTGT 497
QY 485 AGTATGAGGAGGACCAAGAGACCTGTGAAGTCTCTGCTGTGTCCTGACGAGCGAGT 544
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Db 498 AGTATGAGGAGGACCAAGAGACCTGTGAAGTCTCTGCTGTGTCCTGACGAGCGAGT 557
QY 545 GGAGAGGCCCCCGGCTGTCTCTTGAACAGTCCGAAACTTCTGCTGCTCATCAA 604
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 558 GGAGAGGCCCCCGGCTGTCTCTTGAACAGTCCGAAACTTCTGCTGCTCATCAA 616
QY 605 GAACATATCGACTT-CCCGGGCCACAACTACACCAAG- AAACATCTCTGCCAGTTTA 662
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Db 617 GAACATATCGACTTCCCGGGCCACAACTACACCAAGAAACATCTGCCAGTTTA 676
QY 663 AACATCACTGTACCTTCCACAGACTCAGAAATCCACAGTGTCCCAATTTCCGACTAGGA 722
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QY 723 GACATCTCCGAGAAACAGCGGATATTTTTCAGTGTGCGCAATTCAGGCGGGAATATG 782
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Db 737 GACTCTCTC---GGAACAGGCGATA--TTTTCAGATGTGGCA--TCCCGGGGGGATTACT 789
QY 783 GGCATTGAGATCTACTGGGACTG 805
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Db 790 GCGTTCGATCTCTGGGACTG 812

RESULT 4
BG768165      937 bp      mRNA      linear      EST 15-MAY-2001
LOCUS        602744202F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4877137 5',
DEFINITION   mRNA sequence.

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ACCESSION      BG768165
VERSION        BG768165.1 GI:14078818
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 937)
               NIH-MGC http://mgs.nci.nih.gov/.
               National Institutes of Health, Mammalian Gene Collection (MGC)
               Unpublished (1999)
               Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-r@mail.nih.gov
               Tissue procurement: ATCC/DCTD/DTP
               cDNA library preparation: Ling Hong/Rubin Laboratory
               cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
               DNA Sequencing by: Incyte Genomics, Inc.
               Cloning distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               http://image.llnl.gov
               Plate: LLCM1761 row: d column: 02
               High quality sequence stop: 801.
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               /tissue_type="melanotic melanoma, high MDR (cell line)"
               /lab_host="DH10B (phage-resistant)"
               /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
               EcoRI; cDNA made by oligo-dT priming. Directionally cloned
               into EcoRI/XhoI sites using the following 5' adaptor:
               GCCACGAG(G). Size-selected >500bp for average insert size
               1.8kb. Library constructed by Ling Hong in the laboratory
               of Gerald M. Rubin (University of California, Berkeley)
               using ZAP-cDNA synthesis kit (Stratagene) and Superscript
               II RT (Life Technologies). Note: this is a NIH_MGC
               Library."
BASE COUNT     252 a   230 c   249 g   206 t
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Db 49 CGCAGGGAGGAGGCTGTCCACCATGCCGCGCTCTGCGAGCTGCAGTGATGTTTCCAGTA 108
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Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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QY 125 CCACGTGATCATCTTTTCTACCTTTCTTCTGCTGAGTGACAGCTGTACCAGCG 184
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Db 169 CCACGTGATCATCTTTTCTACCTTTCTTCTGCTGAGTGACAGCTGTACCAGCG 228
QY 185 GAAGAGGCTGTATCATCTTTCTGTCACCAAGTGA--GGGATAGCAGAGGTGAAG 243
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Db 229 GAAGAGGCTGTATCATCTTTCTGTCACCAAGTGAAGGGGATAGCAGAGGTGAAG 288
QY 244 AGGAGATCGYGAGAGATGGA--GTGAAGAAAGTGTGTGCACAGTGTCTTTGACACCGCAGA 301
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Db 289 AGGAGATCGTGAGAAATGAGCTGACAGAGTGTGTGTGCACAGTGTCTTTGACACCGCAGA 348
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Db 349 CTACACCTTCCCCTTTTCCAGGGGAAGTCTTCTTCGTGTGATGACAAACTTCTTCAAAACAG 408
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Db 409 AAGGCCACAGACAGCGCTTGTGTCGAGATATCCACCGCAGAGCGTCTTCTTCTCTG 468

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KEYWORDS  
SOURCE

ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 769)  
TITLE  
NIH-MGC http://mgc.nci.nih.gov/  
AUTHORS  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL  
Unpublished (1999)  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC/DCTD/DTF  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LCM1740 row: m column: 01  
High quality sequence stop: 654.

FEATURES  
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/clone.lib="NIH\_MGC\_49"  
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/lab\_host="DH10B (phage-resistant)"  
/note="Organ: skin; Vector: pOB7; Site: 1: XhoI; Site: 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGCAG(G). Size-selected >500bp for average insert size  
1.8kb. Library constructed by Ling Hong in the laboratory  
of Gerald M. Rubin (University of California, Berkeley)  
using ZAP-cDNA synthesis kit (Stratagene) and Superscript  
II RT (Life Technologies). Note: this is a NIH\_MGC  
Library."|"  
BASE COUNT 198 a 189 c 215 g 167 t  
ORIGIN

Query Match 33.4%; Score 619.8; DB 12; Length 769;  
Best Local Similarity 95.2%; Pred. No. 3.2e-156;  
Matches 690; Conservative 3; Mismatches 25; Indels 7; Gaps 5;  
QY 5 CGCAGGAGGAGGCTGCACCATCGCGGCTGTCGACGTCGACGATGATGTTCCAGTA 64  
DB 49 CGCAGGAGGAGGCTGCACCATCGCGGCTGTCGACGTCGACGATGATGTTCCAGTA 108  
QY 65 TGAGAGCAACAAGTCACTCGGATCCAGAGCATGAATATGGACCATTAAGTGTCTT 124  
DB 109 TGAGAGCAACAAGTCACTCGGATCCAGAGCATGAATATGGACCATTAAGTGTCTT 168  
QY 125 CCAGCGATCACTTTTCCACTGTTGCTTCTGCTGAGTGCACAGCTGACCGG 184  
DB 169 CCAGCGATCACTTTTCCACTGTTGCTTCTGCTGAGTGCACAGCTGACCGG 228  
QY 185 GAAAGAGCCTGTCACTAGTCTGTGCACACCAAGGTGAAGGGATACAGAGTGAAGA 244  
DB 229 GAAAGAGCCTGTCACTAGTCTGTGCACACCAAGGTGAAGGGATACAGAGTGAAGA 288  
QY 245 GGAGATCGGAGATGAGTGAAGA-GAAGTGTGTCACAGTCTTTTGACACCGCAGACT 303  
DB 289 GGAGATCGGAGATGAGTGAAGGACGCTTGTGTGATGACAACTTCTCAGAAACAGAA 348  
QY 304 ACACCTTCCTTTGAGGGGAACTCTTCTGCTGATCAACAACCTTCTCA-AAACAGAA 362  
DB 349 ACACCTTCCTTTGAGGGGAACTCTTCTGCTGATGACAACTTCTCAGAAACAGAA 408  
QY 363 GGCCAAAGACGCGGTTGTGTCGAGATATCCACCCGAGGAGCTCTTCTCTGAC 422  
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QY 423 CGAGGTTGTAAGAGGATGATGGAGCCCGCAGAGCAAGGAATTCAGACCGGAGGTT 482

Db 469 CCAGGTTGTAAGAGGATGATGGAGCCCGCAGAGCAAGGAATTCAGACCGGAGGTT 528  
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Db 645 AAGAACATATCGCTTCCCGGCGCACAACTACACACGAGAAACATCTGCCAGGTTTA 704  
QY 663 ACATCACTTTGATC-TTCCACAGACTCAAGATCCACAGTGTCCCATTTTCCGACTAGG 721  
Db 705 ACGATCACTTTGATC-TTCCACAGACTCAAGATCCACAGTGTCCCATTTTTCGACTAGG 764  
QY 722 AGACA 726  
Db 765 AGACA 769

RESULT 7  
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LOCUS  
DEFINITION  
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603252308F1 NIH\_MGC\_96 Homo sapiens cDNA clone IMAGE:5304048 5',  
mRNA sequence.  
ACCESSION  
BI598073  
VERSION  
BI598073.1 GI:15491012  
KEYWORDS  
EST.  
SOURCE  
human.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 860)  
NIH-MGC http://mgc.nci.nih.gov/  
TITLE  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL  
Unpublished (1999)  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
Toshiyuki and Piero Carninci (RIKEN)  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
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High quality sequence stop: 711.

FEATURES  
source

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/lab\_host="DH10B"  
/note="Organ: brain; Vector: pBluescriptR (modified  
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); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTT-3',  
size-selected for average insert size 2.3 kb and  
normalized to ROT 5. This is a primary library enriched  
for full-length clones and constructed using the  
Cap-trapper method (Carninci, in preparation). Library  
constructed by M. Brownstein (NIH/NHGRI, National  
Institutes of Health). Note: this is a NIH\_MGC Library."  
BASE COUNT 223 a 211 c 239 g 187 t  
ORIGIN

Query Match 30.4%; Score 564; DB 13; Length 860;

Best Local Similarity 95.9%; Pred. No. 4e-141; Matches 629; Conservative 3; Mismatches 18; Indels 6; Gaps 5;	
QY	5 CGCAGGAGGGAGGCTGTCACCATGCGCGCTGCTGCACCTGCAGTGCATCTTTTCCAGTA 64
Db	112 CGCAGGAGGGAGGCTGTCACCATGCGCGCTGCTGCAGCTGCAGTGCATCTTTTCCAGTA 171
QY	65 TGAGACGAACAAGTCACTCGGATCCAGACGATGAATATGSCACCAATTAAAGTGGTCTT 124
Db	172 TGAGACGAACAAGTCACTCGGATCCAGACGATGAATATGSCACCAATTAAAGTGGTCTT 231
QY	125 CCAGCTGATCATCTTTTCTCTAGCTTTCCTTGTCTGTGTGAGTGACAGCTGTACACGG 184
Db	232 CCAGCTGATCATCTTTTCTCTAGCTTTCCTTGTCTGTGTGAGTGACAGCTGTACACGG 291
QY	185 GAAAGAGCCCTGCATCACTCTCTGTGCACACCAAGTGAAGGGATAGCAGAGGTGAAGA 244
Db	292 GAAAGAGCCCTGCATCACTCTCTGTGCACACCAAGTGAAGGGATAGCAGAGGTGAAGA 351
QY	245 GGAGATCGTGGAGAAATGGAAGTAAGTTGGTGCACAGTCTCTTTGACACCCGACACTA 304
Db	352 GGAGATCGTGGAGAAATGGAAGTGAAGAAAGTTGGTGCACAGTCTCTTTGACACCCGACACTA 411
QY	305 CACCTTCCCTTTGCAGGGGAACCTTTTCCTCTGTGATGACAAACTTCTCAAAACAGAAG 364
Db	412 CACCTTCCCTTTGCAGGGGAACCTTTTCCTCTGTGATGACAAACTTCTCAAAACAGAAG 471
QY	365 CCAAGAGCAGCGGTTGTGTCGGAGTATCCACCCGAGGACGGTCTGTTCCCTCTCACGG 424
Db	472 CCAGAGCAGCGGTTGTGTCGGAGTATCCACCCGAGGACGGTCTGTTCCCTCTCACGG 531
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QY	484 TAGTATATGAAGGGAACAGAGACCTTG-TGAAGTCTCTGCCCTGGTGGTCCCG-ATCGAGCG 541
Db	592 TAGTATATGAAGGGAACAGAGACCTTGTTGAAGTCTCTGCCCTGGTGGTGGTGGTGGTGGT 651
QY	542 AG--TGAAGAGGCCCCCGGGCGTG-CTCTCTTTGAACAGTCCGGAAGAACTTCAGTGTGT 598
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QY	599 CATCAGAACAAATATCGACTTCCCGCGCCACAACACTACACCGAGAAAGAAATCTCTCG 654
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RESULT 8	BG769595	841 bp	linear	EST 15-MAY-2001
LOCUS	BG769595			
DEFINITION	602744503F1 NTH_MGC_49 Homo sapiens cDNA clone IMAGE:4877545.5, mRNA sequence.			
ACCESSION	BG769595			
VERSION	BG769595.1			
KEYWORDS	EST.			
SOURCE	human.			

ORGANISM	<p>Homo sapiens</p> <p>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.</p>
REFERENCE	<p>1 (bases 1 to 841)</p>
AUTHORS	<p>NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a></p>
TITLE	<p>National Institutes of Health, Mammalian Gene Collection (MGC)</p>
JOURNAL	<p>Unpublished (1999)</p>
COMMENT	<p>Contact: Robert Strausberg, Ph.D.</p> <p>Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a></p> <p>Tissue Procurement: ATCC/DCTD/DTF</p> <p>cDNA Library Preparation: Ling Hong/Rubin Laboratory</p> <p>cDNA Library Arrayed by: the I.M.A.G.E. Consortium (LLNL)</p> <p>DNA Sequencing by: Incyte Genomics, Inc.</p> <p>Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a></p>

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High quality sequence stop: 601.

FEATURES  
source

Location/Qualifiers  
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/lab\_host="DH10B (phage-resistant)"  
/note="Organ: skin; Vector: pORF7; Site\_1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGCAG(G). Size-selected >500bp for average insert size  
1.8kb. Library constructed by Ling Hong in the laboratory  
Of Gerald M. Rubin (University of California, Berkeley)  
using ZAP-cDNA synthesis kit (Stratagene) and Superscript  
II RT (Life Technologies). Note: this is a NIH\_MGC  
Library."|

BASE COUNT      224 a    202 c    237 g    178 t

ORIGIN

Query Match                  29.9%; Score 553.8; DB 12; Length 841;  
Best Local Similarity       91.4%; Pred. No. 2.3e-138;  
Matches 694; Conservative    3; Mismatches 50; Indels 12; Gaps 10;

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QY     65 TGAGAGGAACAAGTCACCTCGGATGCCAGCATGAATTATGSCACCATAAGTGGTTCTT 124  
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Db     110 TGAGACGARCAAGTCACCTCGGATGCCAGCATGAATTATGSCACCATAAGTGGTTCTT 169  
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QY     125 CCAGGTGATCACTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 184  
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Db     170 CCAGTGTATCATCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 229  
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QY     185 GAAGAGCTGTCACTACAGTCTGTGACACCAAGGTGAAGGGATACACAGTGTGAAGA 244  
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Db     230 GAAGAGCTGTCACTACAGTCTGTGACACCAAGGTGAAGGGATACACAGTGTGAAGA 289  
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QY     245 GGAGATCGYGGAATGGAGTGAA--GAAGTTGGTGACACAGTGTCT-TTGTACACCGCAG 302  
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Db     290 GGAGATCGTGGAATGGAGTGAGTGACAGAGTGGTGACAGTGTCTTTTGACACCGGAGAC 349  
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QY     303 TACACTTCCTTTGCAAGGGAATCTTTCTTCTGATGACAAAATTTCTCAA-AA-CAGA 361  
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Db     350 TACAGCTTCCTTTGCAAGGGAATCTTTCTTCTGATGACAAAATTTCTCAA-AACAGA 409  
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Db     410 AGGCCAAGACAGCGGTGTGTGTCTCCGAGTATCCCAACCGCAGGAGCGTCTGTACTCT 469  
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QY     420 GACCGAGTTGTA-AAAAGSGATGGATGGACCGCAGACCAAGSAATTACAGCCGGAAG 478  
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Db     470 GAGCGAGTTGTACAAACGGGATGGATGGATGGACCGCAGACCAAGGAA-TCAGACCGGAA 528  
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QY     479 GTGTGTAGTYATGAAGGGAACCAAGAACCTGTGAA--GYCTCTGCGCTGGTCCCCATC 536  
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QY     655 CAGGTTTTAAACA-TCACTTGTACCTTCCCAAGACTTCAGATTCACAGTGTCCCATTTTC 713  
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Db     709 CAGGTTCAAACATCATTTGTACTTCTCCCAAGATTCAGATTCACAGGTTCCCATTTTFA 768  
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(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

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Best Local Similarity 81.7%; Pred. No. 1.9e-123;
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Db 184 AGCCTGTCACTGTCTGTGCACACCAAGGTGAAGGGGATACGAGAGTGAAGAGGAGA 243
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Db 244 TCGYGAGATGAGTGAAGTGTGTGTCACAGTGTCTT-TGACACCGCAGACTACAC 303
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Db 364 GAGCAGCGGTGTGTCCGAGATACCAACCGCTCAGCTGTGTTCCTCTGACCGAG 423
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QY 487 TRYATGAAGGGAACAGAGACCTGTGAAAGTCTCTGCTGTGTCGCCCATCAGGSCAGTGG 546
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QY 607 ACAATATCGACTTCCCGCCACACTACACACGAGAAACATCTGCGAGTTTAAACA 666
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QY 667 TCACTTGTACTTCCACAGACTCAGAAATCCACAGTGTCCCATTTCCGACTAGGAGACA 726
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QY 727 TCTTCCGAGAAACAGCGCATATTTTTCAGATGKGCAATTCAGGCGGGAATATGGGCA 786
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DEFINITION mRNA sequence.
ACCESSION BF690388
VERSION BF690388.1 GI:11975796
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KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1022)
AUTHORS NIH-MGC http://mgc.nhl.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Cloning Strategy: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L155 row: C column: 04
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1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
BASE COUNT 223 a 283 c 294 g 222 t
ORIGIN
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Db 595 TGGTGCAGGTGGAAGTGCCTCCATCTCACTCCCTGAGGCGCACAGGTGCTGGAG 536
QY 1512 GCGTGTGCTGCGGAAAAAGCGGGGCGCTGCTGACACACCTCAGAGCTGTTCAGGAAG 1571
Db 535 GAGCTGTGCTGCGGAAAAAGCGGGGCGCTGCTGACACACCTCAGAGCTGTTCAGGAAG 476
QY 1572 CTGTGCTGCTGCGGAAAAAGCGGGGCGCTGCTGACACACCTCAGAGCTGTTCAGGAAG 1631
Db 475 CTGTGCTGCTGCGGAAAAAGCGGGGCGCTGCTGACACACCTCAGAGCTGTTCAGGAAG 416
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Db 415 CTGTGCTGCTGCGGAAAAAGCGGGGCGCTGCTGACACACCTCAGAGCTGTTCAGGAAG 356
QY 1692 TGGCGCTTGGGCTCCCGAGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1751
Db 355 TGGCGCTTGGGCTCCCGAGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 296
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Db 295 AGATCCGGAAGAGTTTCORAGAGTGAAGGGCAGTACAGTGGCTTCAGAGTCCCTAC 236
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QY 1812 TGAAGCCAGGACCGTGGCTCAGCTGTGTAAATCCCACTTTT 1853
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Db 235 TGAAGCCAGGACCGTGGCTCAGCTGTGTAAATCCCACTTTT 194
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VERSION BF347290.1 GI:11294885
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 543)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapb@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA library Preparation: Life Technologies, Inc.
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9429 row: f column: 12
High quality sequence stop: 543.
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ORIGIN
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QY 65 TGAGACAGACAAAGTCACTCGGATCCAGACATGAATATGCGACCATTAAGTGTCTT 124
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Db 169 CCACGTGATCATTCTTCTACGTTGCTTCTGCTGAGTGCACAGCTGACCAGC 227
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QY 185 GAAGAGCCCTGTATCAGTTCTGTGCACACCAAGTGAAGGGATAGCAGAGTGAAGA 244
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QY 245 GGAGATCGTGGGAAGTGAAGAGTGGTGGTGCACAGTGTCTTTGACACCGCAGACTA 304
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Db 288 GGAGATCGTGGAGTGAAGAGTGGTGGCAGAGTGC-TTGACCCGCACTA 346
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QY 305 CACCTTCCCTTCAGAGGGAACCTTTCTTCGTGATGACAAAATTTCTCAAACAGAGG 364
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QY 365 CCAAGACAGCGGTTGTGTCGGAGTATCCACCCGAGGAGCTCTGTTCTCTGACCG 424
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QY 425 AGGTTGTAAAAGAGGATGATGACCCCGAGAGCAAGGAATTCAGAC 472
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RESULT 13
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DEFINITION H4027E01 5', mRNA sequence.
ACCESSION BQ554327
VERSION BQ554327.1 GI:21455215
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 642)
AUTHORS VanBuren.V., Piao.Y., Dudekula,D.B., Qian.Y., Carter.M.G., Martin
P.R., Stagg,C.A., Bassey,U., Aliba.K., Hamatani,T., Kargul.G.J.,
Luo.A.G. and Ko.M.S.H.
TITLE Assembly, verification, and initial annotation of NIA 7.4K mouse
cDNA clone set
JOURNAL Unpublished (2002)
COMMENT Other ESTs: H4027E01-3
Contact: Yong Qian
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
Email: cdnaelg@sun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit http://lgsun.grc.nia.nih.gov/cDNA/NIA_7.4K.html for details.
Plate: H4027 row: E column: 01
Seq primer: -21M13 Reverse
High quality sequence stop: 642
POLYA-No.
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Matches 465; Conservative 3; Mismatches 112; Indels 0; Gaps 0;
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LAM9429 row: g column: 13

High quality sequence start: 39

High quality sequence stop: 541.

## FEATURES

Location/Qualifiers

source

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BASE COUNT 144 a 134 c 154 g 123 t  
ORIGIN

Query Match 20.1%; Score 373; DB 12; Length 555;  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

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Maximum Match 100%  
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

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4	1837.8	99.2	2164	9	BC011913	BC011913 Homo sapi
5	1836.2	99.1	2168	6	AX099420	AX099420 Sequence
6	1429.2	77.1	2011	9	AK090866	AK090866 Homo sapi
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ALIGNMENTS

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VERSION AX427649.1 GI:21537769  
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REFERENCE 1  
AUTHORS Morten J.E.  
TITLE Polymorphisms in the human p2x7 gene  
JOURNAL Patent: EP 1199372-A 2 24-APR-2002;











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DEFINITION Sequence 60 from Patent WO0119988.
ACCESSION AX099420
VERSION AX099420.1 GI:13538536
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SOURCE Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1 (bases 1 to 2168)
AUTHORS Jacobs K., McCoy J.M., Lavallie E.R., Collins-Racie L.A., Evans C.,
Merberg D., Treacy M., Bowman M.R., Spaulding V. and Agostino M.J.
TITLE Secreted proteins and polynucleotides encoding them
JOURNAL Patent: WO 0119988-A 60 22-MAR-2001;
Genetics Institute, Inc. (US)
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VERSION AK090866.1 GI:21749107
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REFERENCE 1
AUTHORS Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S.,
            Fukuzumi, Y., Fujimori, Y., Komiyama, M., Sugiyama, T., Irie, R.,
            Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y.,
            Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H.,
            Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K.,
            Watanabe, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A.,
            Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,
            Nishihara, K., Masuhara, Y., Nagai, K. and Isogai, T.
            NEDO human cDNA sequencing project
            Unpublished
REFERENCE 2 (bases 1 to 2011)
AUTHORS Isogai, T. and Yamamoto, J.
TITLE Direct Submission
JOURNAL Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
            Kazuo-Kamatari, Kisarazu, Chiba 292-0812, Japan
            (E-mail: genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
            NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
            HRI, and Biotechnology Center, National Institute of Technology and
            Evaluation; clone selection for full insert sequencing: HRI and
            RAB; annotation: HRI and RAB.
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Best Local Similarity 93.7%; Pred. NO. 0;
Matches 1516; Conservative 15; Mismatches 3; Indels 84; Gaps 1;
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Db 154 GGGGAATCTTCTTCGTGATGACAACTTCTCAAAACAGAGCGCCAGAGCGGTT 213
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[illegible]

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RESULT 8
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LOCUS          R.norvegicus mRNA for ATP ligand gated ion channel.
DEFINITION     X95882
ACCESSION      X95882
VERSION        X95882.1 GI:1322004
KEYWORDS       P2X receptor; P2X7 gene.
SOURCE         Rattus norvegicus.
ORGANISM       Rattus norvegicus
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REFERENCE
AUTHORS        Surprenant,A., Rassendren,F., Kawashima,E., North,R.A. and Buell,G.
TITLE          The cytolitic P2X receptor for extracellular ATP identified as a
                P2X receptor (P2X7)
JOURNAL        Science 272 (5262), 735-738 (1996)
MEDLINE        96202420
PUBMED        8614837

REFERENCE
AUTHORS        Buell,G.N.
TITLE          Direct Submission
JOURNAL        Submitted (26-FEB-1996) G.N. Buell, Glaxo, Molecular Biology, 14
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QY 71 GAACAAAGTCACTCGGATCCAGAGCATGAATATGCGACCAATTAAGTGTCTTCCACGT 130
DB 71 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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 DEFINITION  
 ACCESSION AJ009823  
 VERSION AJ009823.1 GI:4007637  
 KEYWORDS P2X7 gene; P2X7 receptor subunit.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 1810)  
 Simon, J.  
 Direct Submission  
 Submitted (28-JUL-1998) Simon J., Department of Pharmacology,  
 University of Cambridge, Glaxo Institute of Applied Pharmacology,  
 Tennis Court Road, Cambridge, CB2 1QJ, UNITED KINGDOM  
 2 (bases 1 to 1810)  
 Chessell, I.P.; Simon, J.; Hibell, A.D.; Michel, A.D.; Barnard, E.A. and  
 Humphrey, P.P.A.  
 Cloning and Functional Characterisation of the mouse P2X7 receptor  
 FEBS Lett. 4390, 260-300 (1990)  
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## RESULT 10

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 VERSION AC011216.4 GI:8072519  
 KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,

Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhgalter,B.,

Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,

Cooke,P., DeArrellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,

Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,

Galagan,J.C., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,

Lehoczy,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,

McEwan,P., McTurk,A., McKernan,C.H., McLaughlin,J., Meldrum,J.,

Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,

Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,

Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,

Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,

Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.

Direct Submission

Submitted (03-OCT-1999) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

On May 25, 2000 this sequence version replaced gi:7272137.

All repeats were identified using RepeatMasker:

Smith, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIPR

Web site: http://www-seq.wi.mit.edu

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Contact: sequence\_submissions@genome.wi.mit.edu  
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 Center clone name: 6\_F\_18  
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 Sequencing vector: M13; M7815; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.960731  
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 Consensus quality: 165583 bases at least Q30  
 Consensus quality: 167452 bases at least Q20  
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 Insert size: 169065; sum-of-contigs  
 Quality coverage: 4.7 in Q20 bases; agarose-fp  
 Quality coverage: 5.0 in Q20 bases; sum-of-contigs

\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 21 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
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 3778 6053: contig of 2276 bp in length  
 6054 6153: gap of 100 bp  
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## RESULT 12

AC069209  
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 SEQUENCE, 7 unordered pieces.  
 AC069209  
 VERSION  
 KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP; HTGS\_ACTIVEFIN.  
 SOURCE human.  
 ORGANISM Homo sapiens

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 228935)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,  
 Alsbrooks, S.D., Amarantunga, H.C., Are, J.R., Ayele, M., Banks, T.,  
 Barbarella, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D.,  
 Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,  
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 Hernandez, O., Hodgson, A., Hoques, M., Holloway, C., Hollins, B.,  
 Homisi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,  
 Jacobson, B., Jia, I., Johnson, R., Jolivet, S., Joudah, S.,  
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Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Lounsegh, H.,  
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 Tansley, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,  
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 Weinstein, G., and Gibbs, R.  
 Direct Submission  
 Unpublished  
 2 (bases 1 to 228935)  
 Worley, K.C.  
 Direct Submission  
 Submitted (22-MAY-2000) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 228935)  
 Worley, K.C.  
 Direct Submission  
 Submitted (31-JUL-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 On Jul 25, 2002 this sequence version replaced gi:21908286.  
 ----- Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Drafting Center Code: BCM  
 Contact: hgsc-help@bcm.tmc.edu  
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 Consensus quality: 227917 bases at least Q40  
 Consensus quality: 228951 bases at least Q30  
 Consensus quality: 229319 bases at least Q20  
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 Quality coverage: 11x in Q20 bases; sum-of-contigs estimation  
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 \* NOTE: Estimated insert size may differ from sequence length  
 \* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 7 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
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Best Local Similarity 97.4%; Pred. No. 8.7e-124;

Matches 528; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

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Db 105300 TT 105301

RESULT 13

AF083073

LOCUS

AF083073 Bos taurus P2X7 mRNA, partial cds.

DEFINITION

AF083073.1 GI:5880352

ACCESSION

AF083073.1

VERSION

1 (bases 1 to 504)

KEYWORDS

ORGANISM

Bos taurus.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovidae; Bovinae; Bos.

REFERENCE

Smith, R.A. and Estes, D.M.

TITLE

JOURNAL

Submitted (07-AUG-1998) Veterinary Pathobiology, University of

Missouri, 201 Connaway Hall, Columbia, MO 65211, USA

FEATURES

Location/Qualifiers

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/cell\_line="bovine aortic endothelial cell"

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TCEVETWC"

BASE COUNT 138 a 106 c 138 g 122 t

ORIGIN

Query Match 21.1%; Score 390.2; DB 4; Length 504;

Best Local Similarity 85.7%; Pred. No. 1e-88;

Matches 431; Conservative 2; Mismatches 70; Indels 0; Gaps 0;

QY 27 ATGCCGGCTGTGTCAGCTGCAGTGTGTTTCCAGTATGACAGACAAAGTCACTCGG 86

|||

Db 1 ATGCCGGCTGTGTCAGCTGCAGTGTGTTTCCAGTATGACAGACAAAGTCACTCGG 60

QY 87 ATCCAGAGCATGAATATGACCATTAAGTGTGTTTCCAGTATGACAGACAAAGTCACTCGG 146

|||

Db 61 ATCCAGAGCATGAATATGACCATTAAGTGTGTTTCCAGTATGACAGACAAAGTCACTCGG 120

QY 147 GTTTGCTTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 206

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Db 121 ATTGGCTTTGCTTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 180

QY 207 GTSCACACCAAGTGAAGGAGTACAGAGTGAAGGAGTGAAGGAGTGAAGGAGTGAAGGAGT 266

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Db 181 GTSCACACCAAGTGAAGGAGTGAAGGAGTGAAGGAGTGAAGGAGTGAAGGAGTGAAGGAGT 240

QY 267 AAGAAGTGTGTCAGAGTGTGTCAGAGTGTGTCAGAGTGTGTCAGAGTGTGTCAGAGTGTGTCAG 326

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Db 241 AAGAAGTGTGTCAGAGTGTGTCAGAGTGTGTCAGAGTGTGTCAGAGTGTGTCAGAGTGTGTCAG 300

QY 327 TCCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 386

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Db 301 TCCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360

QY 387 GAGTATCCCGCCAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 446

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Db 361 GAGTATCCCGCCAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420

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QY 507 ACTGTGAAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 529

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Db 481 ACTGTGAAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 503

RESULT 14

AC130133/c

LOCUS

AC130133 115282 bp DNA linear HTG 08-AUG-2002

DEFINITION

Rattus norvegicus clone CH230-83K8, \*\*\* SEQUENCING IN PROGRESS \*\*\*

56 unordered pieces.

ACCESSION

AC130133

VERSION

AC130133.1 GI:22138361

KEYWORDS

HTG; HTGS\_PHASE1.

SOURCE

Norway rat.

ORGANISM

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE  
AUTHORS

Rattus.  
1 (bases 1 to 115282)  
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,  
Alsbrooks, S.L., Amarantunge, H.C., Are, J.R., Ayele, M., Banks, T.,  
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Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,  
Davilla, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,  
Delaney, K.R., Delgado, O., Denn, A.B., Ding, Y., Dinh, H.H.,  
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,  
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,  
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Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,  
Weinstock, G., and Gibbs, R.

Direct Submission  
Unpublished  
2 (bases 1 to 115282)  
Worley, K.C.

Direct Submission  
Submitted (08-AUG-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
----- Project Information  
Center project name: GHVX  
Center clone name: CH230-83K8  
----- Summary Statistics  
Sequencing vector: Plasmid;  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 56769 bases at least Q40  
Consensus quality: 59422 bases at least Q30  
Consensus quality: 61794 bases at least Q20

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\* NOTE: Estimated insert size may differ from sequence length  
\* (see <http://www.hgsc.bcm.tmc.edu/docs/genbank/draft.data.html>).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 56 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

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* 88540 91366: contig of 2827 bp in length
* 91367 91466: gap of unknown length
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* 94632 97041: contig of 2410 bp in length
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* 97142 99951: contig of 2810 bp in length
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* 107841 107940: gap of unknown length
* 107941 110756: contig of 2816 bp in length
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DB 105285 GGTCCAGGACAGCCAGATTTGGTCCAGTGTGAAGTGTCCCTCCCTCAACTACAG 105226
QY 1492 AGGCCACAGTGCCTGGAGGCTGTCTCTCCGGAAAGACCGGGGCTGCGATACCA 1551
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QY 1612 ACCAGGACCTTCTGCTGCGCTGTGTGATGTGGAATTCACACAGCCGCTGGGCGCATGTG 1671
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DB 104985 TGCCCAAGCTGCTGCCGCTGGAGATCCGGAAGAGTTCCTCCAGACCCAGGGCAGTACA 104926
QY 1792 GTGGCTTCAAGAGTCTCTACTGA 1814
DB 104925 GTGGCTTCAAGTATCCCTACTGA 104903

RESULT 15
LOCUS AC117579 66872 bp DNA linear HTG 18-MAY-2002
DEFINITION Mus musculus clone RP23-37P22, LOW-PASS SEQUENCE SAMPLING.
ACCESSION AC117579
VERSION AC117579.2 GI:20976671
KEYWORDS HTG; HTGS_PHASE0.
SOURCE Mus musculus.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 66872)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Bookshalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Choepel,Y., Collangelo,M., Collins,S., Collymore,A.,
Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gordon,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kanat,A., Karatas,A., Kells,C., Labrecque,K., Lamazares,R.,
Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K., Liu,G.,
Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L.,
Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,N., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupack,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,
Totham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Willson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (10-APR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE 3 (bases 1 to 66872)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L.,
Bookshalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Choepel,Y., Collangelo,M., Collins,S., Collymore,A.,
Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gordon,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kanat,A., Karatas,A., Kells,C., Labrecque,K., Lamazares,R.,
Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K., Liu,G.,
Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L.,
Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,N., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S.,
Schupack,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,
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Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

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Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S.,  
Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J.,  
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,  
Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

# TITLE JOURNAL

## COMMENT

Submitted (18-Mar-2003) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On May 18, 2002 this sequence version replaced g1:20128322.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RX/RepeatMasker.html>

-----  
Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

----- Project Information

Center project name: L22320

Center clone name: 37\_P\_22

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\* NOTE: This record contains 85 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

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1488 1587: gap of 100 bp  
1588 2264: contig of 677 bp in length  
2265 2364: gap of 100 bp  
2365 3042: contig of 678 bp in length  
3043 3142: gap of 100 bp  
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\* 41782 42461: contig of 680 bp in length  
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Query Match 18.7%; Score 345.6; DB 2; Length 66872;  
Best Local Similarity 79.4%; Pred. No. 3.8e-77;  
Matches 405; Conservative 3; Mismatches 102; Indels 0; Gaps 0;

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Job time : 4814 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 18, 2003, 15:40:30 ; Search time 444 Seconds  
(without alignments)  
9398.543 Million cell updates/sec

Title: US-09-977-221-2

Perfect score: 1853

Sequence: 1 aaacgcaggaggagggct.....cgtctgtaatccacacctttt 1853

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1846.6	99.7	1853	24	AA143027 Human P2X7 gene co
2	1845	99.6	1853	22	AAC63694 Human P2X7/P22 co
3	1836.2	99.1	2168	22	AAF98411 Human cDNA clone C
4	1833.4	98.9	2169	19	AAV30932 Human secreted pro
5	1282.4	69.2	3540	22	AAC63693 Rat P2X7/P22 codi
6	237	12.8	1762	19	AAV27197 HPUR nucleic acid
7	235.4	12.7	1206	22	AAH25211 Nucleotide sequenc
8	235.4	12.7	1759	18	AAV09307 Human brain P2X-1
9	234.6	12.7	1997	17	AAT33853 Rat superior cervi

10	233.8	12.6	1207	22	AA04979 Human purinergic r
11	227.2	12.3	1807	18	AAV09308 Human brain P2X-2
12	203.8	11.0	2833	24	ABK84338 Human cDNA differe
13	203.8	11.0	2833	24	ABK84338 Pancreas cancer re
14	203.8	11.0	2643	17	AAT33855 Human urinary blad
15	196.4	10.6	294	20	AAV89619 EST clone CO390.
16	168.8	9.1	1784	23	AA576004 DNA encoding novel
17	159.6	8.6	1837	17	AAT33852 Rat vas deferens p
18	148.4	8.0	1272	20	AAH87357 Human P2X3 puriner
19	148.4	8.0	1272	21	AAC64099 Human P2X-3 recept
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23	148	8.0	1243	22	AA04966 Human purinergic r
24	147.4	8.0	4900	24	AA143026 Human P2X7 gene 5'
25	145.8	7.9	1272	22	AA04988 Human P2X3 cDNA 5'
26	142.6	7.7	11366	24	AA143028 Human P2X7 gene in
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28	140	7.6	1421	21	AAZ51322 Human purino recep
29	140	7.6	1421	22	AAH25208 Nucleotide sequenc
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32	138.6	7.5	1240	22	AA04982 Human purinergic r
33	138.4	7.5	1349	21	AAZ51323 Human purino recep
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35	138.2	7.5	1639	23	ABK43717 DNA encoding novel
36	135.6	7.3	1499	21	AAZ51324 Human purino recep
37	135.6	7.3	1499	22	AAH25210 Nucleotide sequenc
38	111.6	6.0	564	22	AA192047 Human polynucleoti
39	111	6.0	1697	19	AAV61833 Coding sequence fo
40	109.4	5.9	1293	19	AAV61832 Coding sequence fo
41	107.8	5.8	1360	22	AA04978 Human purinergic r
42	102.6	5.5	1956	24	ABK09794 Human ovarian tumo
43	102.6	5.5	1986	24	ABK84358 Human cDNA differe
44	101.2	5.5	1973	24	ABN59853 Novel human coding
45	96.8	5.2	878	15	AAQ73761 RP-2 Programmed ce

ALIGNMENTS

RESULT 1	
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ID	AA143027 standard; DNA; 1853 BP.
AC	AA143027;
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DT	08-AUG-2002 (first entry)
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XX	
KW	Human; ds; single nucleotide polymorphism; SNP; P2X7-associated disorder;
KW	Inflammation; immune disease; drug development; genetic marker; gene;
KW	P2X7 gene.
XX	
OS	Homo sapiens.
XX	
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FT	CDS
FT	Location/Qualifiers
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FT	replace (760, G)
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FT	/note= "Single nucleotide polymorphism"









CC represented in AAF98490 - AAF98572 which are specific for the cDNA clones  
CC encoding the secreted proteins.

XX Sequence 2168 BP; 539 A; 583 C; 577 G; 469 T; 0 other;

SQ Query Match 99.1%; Score 1836.2; DB 22; Length 2168;  
Best Local Similarity 98.9%; Pred. No. 0;  
Matches 1829; Conservative 16; Mismatches 4; Indels 0; Gaps 0;

QY	5	CGAGGGAGGAGGTGTCACCATGCGCGGCTGCTGCAGTCGACGTGAGCTGATTTTCAGTA	64
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## RESULT 4

AAV30932

ID AAV30932 standard; DNA; 2169 BP.

XX AC AAV30932;

XX DT 14-SEP-1998 (first entry)

XX DE Human secreted protein CO390\_1 cDNA.

XX KW CO390\_1; secreted protein; protein factor; human; ds.









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Db 302 CAG-----CTCAGGAGAAACTCCCTCTCTGTGTATGACCAACTGA 343  
QY 352 TCAGAAAGAGAGGAGAGAGAGAGGTTGTCTCCGAGTATCCACCCGAGGAGCTCT 411  
Db 344 TCCACCATGAACACAGACAGAGGCTGTGCCCCGAGATCCAGATCGACCACTGTGT 403  
QY 412 GTTCTCTGACCGAGTTGTAAGAGGATGGATGACCGCGAGAGAGAAAGATTCAGA 471  
Db 404 GTAATCAGATGCCAGCTGTACTGCCGGCTCTGCCGACCCACACAGCAACGAGTCCAA 463  
QY 472 CCGAAGGTGTGTAGTATGAAGGAGAACAGAGACCTGTGAAGTCTCTGCTGTGGCC 531  
Db 464 CAGCAGGTGCTGAGCTTCAACGGTCCGTCAAGAGCTGTGAGGTGGCGCTGGTGCC 523  
QY 532 CCATCGAGGAGTGAAGAGGCCCCCGGCTGTCTTGAACAGTCCCGAAACTTCA 591  
Db 524 CGGTGGAGATGACACACAGCTGCCACAACTGCTTTTAAAGGCTGCAGAACTTCA 593  
QY 592 CTGTGCTCATCAGACATATFCGACTTCCCGGGCCACAACTACACACGAGAAATCC 651  
Db 584 CTCCTTTGGTAAAGAACATCTGGTATCCCAATTTAATTTACAGAGAGGAATATCC 643  
QY 652 TGCAGGTTTAAACATCACT-----TGTACTTCCACAGACTCAGAAATCCAC 699  
Db 644 TTCCACATCACCACACTACTTACCTCAAGTCGTGATATGATGCTAAACAGATCCCT 703  
QY 700 AGTGTCCATTTTCGACTAGGAGACATFTCCGAGAGAACAGCGCATATTTTCAGATG 759  
Db 704 TCTGCCCATATTCCTGCTTGGCAAAATAGTGGAGAACGACGACACAGTTCCAGGACA 763  
QY 760 KGGCAATTCAGGCGGAATTAAGGCAATGAGATCTGAGTCTGAGGACTGCAACCTAGACGTT 819  
Db 764 TGGCCGTGGAGGAGGAGCATATGGGCATCCAGGTCAACTGGGACTGCAACCTGGACAGAG 823  
QY 820 GTTTCATCACTCCCTCCCAATACAGTTTCCTGTGCTGTGACGACAGACCCCAACG 879  
Db 824 CCGCTCCCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 883  
QY 880 TGTCTTGTACCTGCTACAACTTCAGATACGCAAGTACTACAGGAAACAAATG--- 936  
Db 884 ACAAGTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 943  
QY 937 TTGAGAAACGAGCTGTGATAAGTCTTCGGGATCCGTTTGCATCTGTTTGGCA 996  
Db 944 ACAGAGAGCCGAGGCTCATCAAGGCTATGGCATCCGCTTCGACATCATTTGTTGGGA 1003  
QY 997 CCGGAGGAAATTTGACATATCCAGCTGTTGTGTACATCGGCTCAACCTCTCCCTACT 1056  
Db 1004 AGGAGGAGAAATTTGACATATCCCACTATGATCAACATCGGCTCTGGCTGGCACTGC 1063  
QY 1037 TCGTCTGGCCCTGTGTTTCATCGACTTTCCTCATC 1091  
Db 1064 TAGGCATGGGACCGTGTGTGATCATATGATC 1098

RESULT 7

AAH25211  
ID AAH25211 standard; DNA; 1206 BP.

AC  
AC  
XX  
XX

DT 22-AUG-2001 (first entry)

XX Nucleotide sequence of a human purinoreceptor P2X4.

KW Human; purinoreceptor; P2X2; P2X4; pain; neuroendocrine disease;  
XX auditory disease; vestibular disorder; ss.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 21..1187  
FT /\*tag= a  
FT /product= "purinoreceptor P2X4"  
XX  
XX US6242216-B1.  
XX PN  
XX PD 05-JUN-2001.  
XX XX  
XX PF 13-NOV-1998; 98US-0191608.  
XX XX 14-NOV-1997; 97US-0065822.  
XX PR 20-AUG-1998; 98US-0137458.  
XX XX  
XX PA (ABBO ) ABBOTT LAB.  
XX PI Lynch KJ, Burgard EC, Metzger RE, Niforatos W, Touma EB;  
XX PI Van Biesen T;  
XX XX  
XX DR WPI: 2001-388837/41.  
XX DR P-PSDB; AAB84382.  
XX  
XX Isolated polynucleotides, used to produce P2X2 receptor polypeptides and  
XX identify potentially therapeutic compounds, encode a human P2X2  
XX receptor polypeptide -  
XX  
XX Example 4; Fig 11; 40pp; English.  
XX  
XX The specification describes nucleic acids encoding a functional human  
XX purinoreceptor polypeptides P2X2 and P2X4. P2X polypeptides and  
XX polynucleotides are used to identify modulators, which may be used to  
XX treat and prevent pain, diseases of the neuroendocrine system, and  
XX auditory and vestibular disorders. P2X and P2X polynucleotides are a  
XX source of probes and primers, which may be used to identify homologous  
XX sequences, for gene localisation studies, and for gene therapy purposes.  
XX The polynucleotides may also be used to produce the polypeptide  
XX recombinantly. The P2X polypeptides are used to arise antibodies, and  
XX to identify inhibitors. The present sequence encodes human P2X4.

XX SQ Sequence 1206 BP; 285 A; 335 C; 320 G; 266 T; 0 other;

Query Match 12.7%; Score 235.4; DB 22; Length 1206;  
Best Local Similarity 54.3%; Pred. No. 3.5e-54;  
Matches 573; Conservative 5; Mismatches 441; Indels 36; Gaps 4;

QY 55 TTTTCCAGTATGAGACGACAAAGTCACCTCGATCCAGACGATGATATGACCACTTA 114  
Db 55 TGTTCGAGTACGACACGCGCGCATCGTCTCATCCGACGCGCAAGTGGGCTCATGA 114  
QY 115 AGTGTGTTCTCCAGGTGATCATCTTTTCTCTAG--TTTGTCTTGTCTGTGAGTACACA 171  
Db 115 ACCGGCGCGTGCACACTGCTCATCTCGGCTACGTCATCGGGTGGGTTGTGGGAAA 174  
QY 172 AGCTGTACACGCGAAGAGCGCTGTGTCATCAGTCTGTGTCACACCAAGGTGAAGGGATAG 231  
Db 175 AGGGCTACCGAGAACTGACTCCGTGGTCACTCCGTTACGACCAAGGTCAAGGCGTGG 234  
QY 232 CAGAGGTGAAGAGGAGATCGTGGAGATGGAGTGAAGAAGTTGGTGCACAGTGTCTTTG 291  
Db 235 CTGTGACCAACACTTCTAAACTTGGATTCCGGATCTGGGATGTGGGATTTATGTGATAC 294  
QY 292 ACACCGCAGACTACACTTCCCTTTTCAGAGGAGACTTTTCTTCGTGATGACAACTTC 351  
Db 295 CAG-----CTCAGAGGAGAAACTCCCTCTTCGTGATGACCAACGTGA 336  
QY 352 TCAGAAAGAGAGGAGAGAGAGCGGTTGTGTCTCCGAGTATCCACCCGAGGAGCTCT 411  
Db 337 TCTTCACCATGACCAAGACAGAGAGGCGCTGTGCCCGGAGATTCAGATGCGACCATGTGT 396







```

Db 777 TCTGCCCATATTCGCTTGGCACAATCGTGGGGACGGGACATAGCTCCAGGAGA 836
Qy 760 KGGCAATTCAGGGGGAATATGGCATTTGAGATCTACTGGGACTGCACCTTAGACCTT 819
Db 837 TGGCAGTTGAGGGAGGATCATGGGTATCCAGATCAAGTGGGACTGCAACCTGGATAG 896
Qy 820 GGTCCACTACTGCTCCCAATACAGTTTCCTTCGCTTGACGACCAAGACCAACG 879
Db 897 CGGCTCCCTTGGCTCCAGATATTCCTCCGGCGCTGGACACCGGGACCTGGAC 956
Qy 880 TGTCTTTGACCTGGCTACAACTCAGATAGCAGATCAAGTACTACAAGG---AACAATG 936
Db 957 ACAATGTGTCTCTGGCTACAACTTTCAGTTTGGCAAGTACTACAGGACCTGGCGCA 1016
Qy 937 TTGAGAACGGACTCATAAAGTCTTCGGATCCGTTTGCATCTCTGGTTTGGCA 996
Db 1017 AAGACGGCAGCACTCACCAGGCTAGGCAATCCGCTTTGATCATCGTGTGGAA 1076
Qy 997 CGGAGGAAATTTGACATATCCAGCTGGTTGTGTATCGGCTCAACCTCTCTACT 1056
Db 1077 AGGCTGGGAAGTTTGACATCATCCCTACCATGATCAAGTTGGCTCTGGCTGGCTCC 1136
Qy 1057 TGGGCTGGGCRCTGTTTCATCGACTCCCTCCTC 1091
Db 1137 TCGGGGTGGCAGGCTGCTCTGTGACGTATAGTC 1171

RESULT 10
RAD04979
ID AD04979 standard; DNA: 1207 BP.
AC AD04979;
DT 17-JUL-2001 (first entry)
DE Human purinergic receptor P2X4 receptor DNA.
KW Human; purinergic receptor; P2X4; antidepressant; vulnary; hypotensive;
KW anticonvulsant; antiinflammatory; therapy; nervous system disorder;
KW epilepsy; pain; depression; neurodegenerative disorder; cystic fibrosis;
KW irritable bowel disorder; reproductive system disorder; hypertension;
KW peripheral vascular disease; immune system disorder; chronic bronchitis;
KW premature ejaculation; asthma; neuromuscular disease; ds.
OS Homo sapiens.
PH Key Location/Qualifiers
FT CDS 21..1186
FT FT /*tag= a
FT FT /product= "Human P2X4 receptor"
FT FT 263
FT FT /*tag= b
FT FT /note= "Represented in the specification as F"
US6214581-B1.
PN 10-APR-2001.
XX 13-NOV-1998; 98US-0191136.
XX 16-JAN-1998; 98US-0071298.
PR 16-JAN-1998; 98US-0071669.
PR 16-JAN-1998; 98US-0008185.
PR 16-JAN-1998; 98US-0008526.
XX (ABBO ) ABBOTT LAB.
XX Lynch KJ, Burgard EC, Van Biesen T;
PI WPI; 2001-315459/33.
XX Novel isolated polynucleotide encoding human purinergic P2X3 receptor

```

```

PT polypeptide useful for identifying potentially therapeutic compounds
PT that modulate or otherwise interact with P2X containing receptors
XX
PS Example 11; Fig 10; 53pp; English.
XX
CC The present sequence is human P2X4 receptor DNA containing its open
CC reading frame with EcoRI restriction used for subcloning. P2X
CC receptors are ligand-gated ion channels while P2X receptors operate
CC generally through a G-protein coupled system. P2X purinoreceptor drugs
CC are potential therapeutic agents in several disorders including central
CC nervous system or peripheral nervous system conditions, e.g., epilepsy,
CC pain, depression, neurodegenerative disorders, disorders of the skeletal
CC muscle such as neuromuscular diseases, disorders of the reproductive
CC system, asthma, peripheral vascular disease, hypertension, immune system
CC disorders, irritable bowel disorder, premature ejaculation, cystic
CC fibrosis and chronic bronchitis. P2X purinoreceptors mediate the activity
CC of extracellular nucleotide triphosphates to regulate chloride secretion
CC in human airway epithelia.
XX
SQ Sequence 1207 BP; 285 A; 335 C; 320 G; 266 T; 1 other;

```

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Query Match 12.68; Score 233.8; DB 22; Length 1207;
Best Local Similarity 54.9%; Pred. No. 9.5e-54;
Matches 581; Conservative 4; Mismatches 432; Indels 41; Gaps 5;
Qy 55 TTTTCCAGTATGACAGCAACAAAGTCACCTCGGATCCAGACATGAATTATGGCACCATTA 114
Db 55 TGTTCGATAGACACGCGCCGCGCATCGTCTATCCCGCAGCCCAAGTGGGGCTCAGA 114
Qy 115 AGTGTCTTCCACGATGATCATCTTTTCTAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 171
Db 115 ACCGGCGCGTCAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 174
Qy 172 AGCTGTACAGCGGAAGACCTGTCTCATCAGTCTGTGTGCACACCAAGTGTGAGGGGATAG 231
Db 175 AGGGCTACCGAAGAACTGACTCCGTGGTGCAGTCCGTGTACGACCAAGTCAAGGCGGTGG 234
Qy 232 CAGAGGTGAAAGAGAGATCGYGGAGAATGGAGTGAAGAAGTGTGTGCACAGTGTCTTTG 291
Db 235 CNGTGACCAAC-----ACITCTAAACTTGGATTCCCGATCTCGG 274
Qy 292 ACACGCGAGTACACCTTCC---CTTTGAGGGGAACTCTTTCTGCGATGACAAACT 348
Db 275 ATGTGCGGATATGTATACAGCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 334
Qy 349 TTCTCAAAACAGAGGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 408
Db 335 TGATCTCACCATGACACGACAGAGGCGCTGTGCCCGGAGATTCAGATGCGGACCATG 394
Qy 409 TCTGTCTCTCTGACCGAGTGTGTAAAGAGGATGGATGGACCGGACAGACAAAGGAATTC 468
Db 395 TGTGTAAATCAGATGCCAGCTGTACTCGGCTCTGCGGCGCACCACACAGAGTCT 454
Qy 469 AGACCGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 528
Db 455 CAACAGGCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 514
Qy 529 GCCCATCGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 588
Db 515 GCCCGTGGAGATGACACACAGTGCACCAACTGTCTTTTAAAGGCTGCAGAAACT 574
Qy 589 TCACCTGTCTCATCAGACAAATATGCTTCCCGGCGCACAACATACACCGAGGAGAAACA 648
Db 575 TCACCTCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 634
Qy 649 TCCTGCCAGTTTAAACATCACT-----TGTACCTTCCACAGACTCAGATC 696
Db 635 TCCTTCCCAACATCACCACACTACTTACCTCAAGTGTGCTATTTATGATGTTAAACAGATC 694
Qy 697 CACAGTGTCCATTTTCCGACTAGAGACATCTTCCGAGAAACAGCGGATATATTTTCAG 756
Db 695 CTTCTGCCCATATTCCTCTTGGCAAAATAGTGGAGAACGAGGACGAGGAGGAGGAGGAGG 754

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RESULT 13	
ABL70017	
ID	ABL70017 standard; DNA; 2633 BP.
XX	
XX	ABL70017;
DT	15-MAY-2002 (first entry)
XX	
DE	Pancreas cancer related gene sequence SEQ ID NO:8354.
XX	
KW	Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW	stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW	cytostatic; gene therapy; anti-neoplastic; Wilms' tumour; adenocarcinoma;
KW	gene; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200194629-A2.
XX	
PD	13-DEC-2001.
PF	
XX	30-MAY-2001; 2001WO-US10838.
XX	
PR	05-JUN-2000; 2000US-209473P.
PR	05-JUN-2000; 2000US-209531P.
PR	18-SEP-2000; 2000US-233133P.
PR	18-SEP-2000; 2000US-233617P.
PR	20-SEP-2000; 2000US-234009P.
PR	20-SEP-2000; 2000US-234034P.
PR	20-SEP-2000; 2000US-234052P.
PR	22-SEP-2000; 2000US-234503P.
PR	22-SEP-2000; 2000US-234508P.
PR	22-SEP-2000; 2000US-234567P.
PR	25-SEP-2000; 2000US-234923P.
PR	25-SEP-2000; 2000US-234924P.
PR	25-SEP-2000; 2000US-235077P.
PR	25-SEP-2000; 2000US-235082P.
PR	25-SEP-2000; 2000US-235133P.
PR	25-SEP-2000; 2000US-235280P.
PR	26-SEP-2000; 2000US-235637P.
PR	26-SEP-2000; 2000US-235638P.
PR	27-SEP-2000; 2000US-235711P.
PR	27-SEP-2000; 2000US-235720P.
PR	27-SEP-2000; 2000US-235840P.
PR	27-SEP-2000; 2000US-235863P.
PR	28-SEP-2000; 2000US-236028P.
PR	28-SEP-2000; 2000US-236029P.
PR	28-SEP-2000; 2000US-236033P.
PR	28-SEP-2000; 2000US-236034P.
PR	28-SEP-2000; 2000US-236109P.
PR	28-SEP-2000; 2000US-236111P.
PR	29-SEP-2000; 2000US-236642P.
PR	29-SEP-2000; 2000US-236891P.
PR	02-OCT-2000; 2000US-237172P.
PR	02-OCT-2000; 2000US-237173P.
PR	02-OCT-2000; 2000US-237278P.
PR	02-OCT-2000; 2000US-237294P.
PR	02-OCT-2000; 2000US-237295P.
PR	02-OCT-2000; 2000US-237316P.
PR	03-OCT-2000; 2000US-237425P.
PR	03-OCT-2000; 2000US-237598P.
PR	03-OCT-2000; 2000US-237604P.
PR	03-OCT-2000; 2000US-237606P.
PR	03-OCT-2000; 2000US-237608P.
PR	01-NOV-2000; 2000US-244867P.
PR	01-NOV-2000; 2000US-245084P.
XX	
PA	(AVAL-) AVALON PHARM.
XX	
XX	Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI	Soppet DR, Weaver Z;
XX	
DR	WFI; 2002-188264/24.

Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set -

Claim 1; SEQ ID 8354; 44pp; English.

The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL701110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms' tumour.

Sequence 2633 BP; 582 A; 804 C; 701 G; 546 T; 0 other;

Query Match	11.0%;	Score 203.8;	DB 24;	Length 2633;
Best Local Similarity	54.8%;	Prod. No. 2.5e-45;		
Matches 447;	Conservative	5;	Mismatches 342;	Indels 21; Gaps 2;
QY	285	GTCTTTGACACGCGAGACTACACCTTCCCTTTTCGAGGGAACTCTTCTTCGTGTGATGACA	344	
Db	446	GTCTGGGATGTGGCTGATCTAGCTTCTCCAGCCAGGGGGCACTCTCTTCGTGTGTCATG	505	
QY	345	AACCTTCTTCATAAACAGAAGGCCAAGACGACGGTGTGTCTCCGAGTAGTATCCACACCCGACGG	404	
Db	506	ACCAATTTTCATCGTGACCCCGAAGCAGACTCAAGGCTACTGCGCAGAGACACCCAGAAGGG	565	
QY	405	ACGCTCTGTTCCTCTGACCGAGGTTGTAAAAAGGATGATGGACCGCAGACAGCAAGGA	464	
Db	566	GGCATATGCAAGGAAGACAGCTGGCTGTACCCCTTGGGAAGGCCAAGAGAAAGGCCCAAGC	625	
QY	465	ATTACAGACCGGAGGTGTGTAGTATGAAGGGAAACAGAGACCTGTGAAGTCTCTGCC	524	
Db	626	ATCCGACGGGCAAGTGTGTGGCCTTCAACGACACTGTGAGACGTGTGAGATCTTTTGGC	685	
QY	525	TGSGTGCCCATCGAGCGCAGTGGAAAGAGGCCCCCGCGCTGTCTCTTTGAACAGTCCGGAA	584	
Db	686	TGSGTGCCCGTGGAGGTGGATGACGACATCCCGCGCGCTGCCCTCTCCGAGAGGCGCGAG	745	
QY	585	AACCTTCAGTGTCTCATCAAGAACAATATCGACTTCCCGGGCCCAACATCACACAGCA	644	
Db	746	AACCTTCAGTCTTTTCATCAAGAACAGCATCAGCTTCCACGCTTCAAGGTCACACAGGCGC	805	
QY	645	AACATCTGCGCAGGTTTAAA-----CATCACTTGTAGCTTCCACAGACTCAG	692	
Db	806	AACCTGTGGAGGAGGTGAATGCTTGCCCATCAAGACCTGCCTCTTTCACAGACCCCTG	865	
QY	693	AATCCACAGGTGCCATTTTCCGACTAGGAGACATCTTCCGAGAAACAGGCGGATAATTTT	752	
Db	866	CACCCCTGTGCCAGTCTTCCAGCTTGGCTACGTGGTGCAAGAGTCAAGGCCAGAACTTC	925	
QY	753	TCAGATGKGCAATTCACGGCGGGAATAATGGGCAATGAGATCTACTGGGACTGCAACCTA	812	
Db	926	AGCACCTGTGCTGAGAAGGGTGGAGTGGGCTACCATCGACTGGCACTGTGACCTGTGACCTG	985	
QY	813	GACCGTTGGTTCATCACTGCGCTCCCAATAACAGTTTTCCTGCGCTTGACGACAGAAC	872	
Db	986	GACTGGCAACGTAGGCATCGCAGACCCCATCTATGAGTTCATGGGCTGTACGAGAGAA	1045	
QY	873	ACCAACGTGTCTTGTATCCCTGGCTCAACTTCAGATACGCCAAGTACTACAGAGAAAC	932	

Db 1046 A-----AFCCTCCAGGCTTCAACTTCAGTTTGCCAGGCATTTGTGGAGAC 1096  
 QY 933 AATGTTGAGAAAGGACTCTGATAAAAGTCTTCGGGATCCGTTTGTGACATCTGTTT 992  
 Db 1097 GGGACCACTACCGTCACTTCTCAAGGTTTGGGATTCGCTTTGACATCTGTTGGAC 1156  
 QY 993 GGCACCGGAGGAAAATTGACATATCCAGCTGGTGTGTACATCGGCTCAACCCCTCTCC 1052  
 Db 1157 GGCACGGCGGGAAGTTTGACATCATCCCTACAATGACCACCACTCGGCTGTGATTCGC 1216  
 QY 1053 TACTTCGCTGCGCCCTGTGTTCAATCGACTTCCT 1087  
 Db 1217 ATCTTTGGGTGGCCACAGTCTCTGTGACCTGCT 1251

## RESULT 14

AAT33855  
 ID AAT33855 standard; cDNA; 2643 BP.

XX AC AAT33855;

XX DT 23-NOV-1996 (first entry)

XX DE Human urinary bladder P2x receptor cDNA.

KW ATP P2x receptor; purinoceptor; ligand-gated ion channel; agonist;  
 KW antagonist; epilepsy; cognition; emesis; pain; asthma;  
 KW peripheral vascular disease; hypertension; irritable bowel syndrome;  
 KW premature ejaculation; cystitis; therapy; ss.

OS Homo sapiens.

XX Key Location/Qualifiers  
 FT CDS 174..1373  
 FT /\*tag= a

XX PN W09533048-A2.

XX PD 07-DEC-1995.

XX PF 24-MAY-1995; 95WO-EP01968.

XX PR 09-FEB-1995; 95GB-0002480.

XX PR 27-MAY-1994; 94GB-0010664.

XX PA (GLAX ) GLAXO GROUP LTD.

XX PI Buell GN, Valera S;

XX PS WPI; 1996-030561/03.

XX DR P-PSDB; AAW04218.

XX CC DNA encoding ATP P2x receptors of the purinoceptor family - for  
 XX screening cpds. useful in treating epilepsy, cognition, emesis,  
 XX pain, asthma, peripheral vascular disease, hypertension, etc.

XX PS Claim 1; Fig 4; 82pp; English.

XX CC A cDNA clone (AAT33855) codes for the human urinary bladder P2x  
 XX receptor (AAW04218), a ligand-gated ion channel that opens upon  
 XX binding of extracellular ATP. It was isolated from a bladder  
 XX cDNA library using a rat smooth muscle P2x receptor probe.  
 XX Rat vas deferens, superior cervical ganglion and dorsal root  
 XX ganglion P2x receptor cDNAs (AAT33852-54) have also been isolated.  
 XX These cDNAs can be used to produce recombinant P2x receptors in  
 XX host, esp. mammalian, cells for use in screening (ant)agonist  
 XX cpds.

XX SQ Sequence 2643 BP; 607 A; 794 C; 701 G; 541 T; 0 other;

XX Query Match

XX Best Local Similarity 11.0%; Score 203.8; DB 17; Length 2643;

XX Matches 447; Conservative 5; Mismatches 342; Indels 21; Gaps 2;

QY 285 GTCTTTGACACCGCAGACTACACTTTCCTCTTGACGGGGAACCTCTTCTTCGTGATGACA 344  
 Db 423 GTCTGGGATGTGGTGAAGTCTTCCAGCCAGGGGGACAACTCTCTCGTGTGATG 482  
 QY 345 AACTTTCTCAAAACAGAAAGCCCAAGAGCAGAGCGGTTGTCTCCCGAGTATCCCAACCGCAGG 404  
 Db 483 ACCAATTCATCGTGACCCCGAAGCAGACTCAAGCTACTGCGCAGAGCACCCAGAGGG 542  
 QY 405 AGCTCTGTCTCTGACCCAGGTTGTAATAAAGGATGGATGGAGCCCGCAGAGCAAGAGA 464  
 Db 543 GGCATATGCAAGGAAGACAGTGTCTACCCCTGGGAAGGCCAAGAGGAAGGCCAAGGC 602  
 QY 465 ATTACAGACCGGAAGTGTGTAGTATGAAGGAACAGAGAACCTGTGAAGTCTCTCC 524  
 Db 603 ATCCGACGGCAAGTGTGTGGCTTCAACGACACTGTGAAGACGTGTGAGATCTTTGGC 662  
 QY 525 TGGTCCCCCATCGAGGCACTGGAAGAGGCCCGCCCGGCTGCTCTCTTTGAACAGTCCCGAA 584  
 Db 663 TGGTGGCCCGTGGAGTGGATGACGACATCCCGCGCCCTGCCCTTCTCCGAGAGGCCGAG 722  
 QY 585 AACTTCACCTGTCTCATCAGAAACATATCAGACTTCCCGGCCACACACTACACACGAGA 644  
 Db 723 AACTTCACCTCTTTTCATCAAGAAACAGCATCAGCTTTCACGCTTCAAGGTCAACAGGCC 782  
 QY 645 AACATCCCTCCAGGTTTAAA-----CATCACTTGTACTTCCACAGACTCAG 692  
 Db 783 AACTTGGTGGAGAGGTGAATGCTGCCACATGAAGACCTGCTCTTTCAGAAACCTTG 842  
 QY 693 AATCCACAGTGTCCATTTCCGACTAGAGACATCTTCGAGAAACAGGCGATTAATTTT 752  
 Db 843 CACCCCTGTGCCAGTCTTCCAGCTTGGCTACGTGGTGCAGAGTCAAGAGTCAAGGCAACTTC 902  
 QY 753 TCAGATGKGCATTCAGGGCGGAATAATGGSCATGTGAGATCTACTGGGACTGCAACCTA 812  
 Db 903 AGCACCTGGCTGAGAAGGGTGGAGTGGCATCACCATCGACTGGGACTGTGACCTG 962  
 QY 813 GACCGTTGGTTCATCACTGCCCTCCCAATAACAGTTTCCCTCGCCTTGACACAGAGACC 872  
 Db 963 GACTGGCAGTACGGCACTGCAGACCACTATGAGTTCATGGCTGTACGAAGAGAA 1022  
 QY 873 ACCACAGTGTCTGTACCTCGCTACAACCTCAGATAGCCAGTACTACAGAGAAAC 932  
 Db 1023 A-----ATCTCTCCCGAGGCTTCAACTTCAGTTTGCAGGCACTTTGTGAGAAC 1073  
 QY 933 AATGTTGAGAAACGCACTGTGATAAAGTCTTCGGGATCCGTTTGTACATCTCTGGTTT 992  
 Db 1074 GGGACCACTACCGTCACTTCAAGGTGTTGGGATTCGTTGACATCTGTGGGAC 1133  
 QY 993 GGCACCGGAGGAAATTTGACATATCCAGTGGTGTGTACATCGGCTCAACCCCTCTCC 1052  
 Db 1134 GGCAGGCGGGGAAGTTTGACATCATCCCTACAATGACCACCATCGGCTCTGGAATTGGC 1193  
 QY 1053 TACTTCGCTGTGGCCCTGTGTGTTCACTCGACTTCCT 1087  
 Db 1194 ATCTTTGGGTGGCCACAGTCTCTGTGACCTGCT 1228

## RESULT 15

AAV89619

ID AAV89619 standard; cDNA; 294 BP.

XX AC AAV89619;

XX DT 15-FEB-1999 (first entry)

XX DE EST clone CO390.

XX KW Human; secreted protein; expressed sequence tag; EST; haematopoiesis;

XX KW tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic;

XX KW receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;

XX gene therapy; ss.

OS	Homo sapiens.
XX	
PN	W09845436-A2.
XX	
PD	15-OCT-1998.
XX	
PF	10-APR-1998; 98WO-US06955.
XX	
PR	10-APR-1997; 97US-0838821.
XX	
PA	(GEMV ) GENETICS INST INC.
XX	
PI	Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;
PI	Racie LA, Spaulding V, Treacy N;
XX	
DR	WPI; 1999-070077/06.
XX	
PT	New polynucleotides encoding human secreted proteins - derived from
PT	e.g. human blood, kidney, foetal lung, placenta, testes, brain,
PT	ovary, pituitary, retina and colon cDNA libraries.
XX	
PS	Claim 1; Page 276; 618pp; English.
XX	
CC	The present sequence represents a human expressed sequence tag (EST).
CC	The polynucleotide, which is a secreted EST, and the encoded protein
CC	are predicted to have useful biological activities which would make
CC	them suitable for treating, preventing or ameliorating medical
CC	conditions in humans and animals, although no supporting data is
CC	given. Suggested activities include nutritional activity, immune
CC	stimulating or suppressing activity, haematopoiesis regulating
CC	activity, tissue growth activity, activin/inhibin activity,
CC	chemotactic/chemokinetic activity, haemostatic and thrombolytic
CC	activity, receptor/ligand activity, anti-inflammatory activity,
CC	cadherin/tumour invasion suppressor activity, tumour inhibition
CC	activity. The polynucleotide may also be useful for gene therapy.
XX	
SQ	Sequence 294 BP; 81 A; 72 C; 68 G; 73 T; 0 other:
	Query Match            10.6%; Score 196.4; DB 20; Length 294;
	Best Local Similarity    98.5%; Pred. No. 9e-44;
	Matches 197; Conservative    1; Mismatches    2; Indels    0; Gaps    0;
QY	576 AGTCGGCGAAACACTTCACTGTGCTCATCAAGACAATATCGACTTCCC GGCCCACTAC 635 
Db	30 AGTCGGCGAAACACTTCACTGTGCTCATCAAGACAATATCGACTTCCC GGCCCACTAC 89 
QY	636 ACCACAGAGAACAATCCTGCCAGGTTTAAACATCACWTGTACCTTCCACAGACTCAGAA 695 
Db	90 ACCACAGAGAACAATCCTGCCAGGTTTAAACATCACWTGTACCTTCCACAGACTCAGAA 149 
QY	696 CCACAGTGTCCTATTTCGCAGTAGGAGACATCTTCCGAGAAACAGGCGATAATTTTCCA 755 
Db	150 CCACAGTGTCCTATTTCGCAGTAGGAGACATCTTCCGAGAAACAGGCGATAATTTTCCA 209 
QY	756 GATKGCAATTCAGGGGG 775 
Db	210 GATGGCAATTCAGGTTGG 229 





QY 361 AAGCCAAAGACAGCGGTTGTCCCGAGTATCCACCCGCGAGGAGCTCTGTCTCTCTG 420  
DB 361 AAGCCAAAGACAGCGGTTGTCCCGAGTATCCACCCGCGAGGAGCTCTGTCTCTCTG 420  
QY 421 ACCGAGGTTGTAAGAGGATGGATGGACCCGAGAGCAAGAAATTCAGACCGGAAGGT 480  
DB 421 ACCGAGGTTGTAAGAGGATGGATGGACCCGAGAGCAAGAAATTCAGACCGGAAGGT 480  
QY 481 GTGTAGTATYATGAGAGGAAACAGAGACCTGTGAAGTCTGTGCTGGTGGCCCATCGAGG 540  
DB 481 GTGTAGTATYATGAGAGGAAACAGAGACCTGTGAAGTCTGTGCTGGTGGCCCATCGAGG 540  
QY 541 CAGTGAAGAGCCCGCCGCGCTCTCTTGAACAGTGGCGGAAACTCACTGTGCTCA 600  
DB 541 CAGTGAAGAGCCCGCCGCGCTCTCTTGAACAGTGGCGGAAACTCACTGTGCTCA 600  
QY 601 TCAGAGCAATATGCACTTCCCGGCGCAACTACACAGAGAAACATCCCGCAGGTT 660  
DB 601 TCAGAGCAATATGCACTTCCCGGCGCAACTACACAGAGAAACATCCCGCAGGTT 660  
QY 661 TAAACATCACTGTACCTTCCACAGACTCAGAAATCCACAGTGTCCCATTTCCGACATG 720  
DB 661 TAAACATCACTGTACCTTCCACAGACTCAGAAATCCACAGTGTCCCATTTCCGACATG 720  
QY 721 GAGACATCTCCGAGAAACAGGCGATAATTTTCAGATGKGCAATTCAGGCGGGAATAA 780  
DB 721 GAGACATCTCCGAGAAACAGGCGATAATTTTCAGATGKGCAATTCAGGCGGGAATAA 780  
QY 781 TGGGATTCAGATCTAGGACTGCAACTAGACGCTTGGTTCCATFCACTGCGCTCCCA 840  
DB 781 TGGGATTCAGATCTAGGACTGCAACTAGACGCTTGGTTCCATFCACTGCGCTCCCA 840  
QY 841 AATACAGTTTCRCGCTTGACGACAGCAAGCAACCAAGCTGCTGTGCTGCTGCTGCTACA 900  
DB 841 AATACAGTTTCRCGCTTGACGACAGCAAGCAACCAAGCTGCTGTGCTGCTGCTGCTACA 900  
QY 901 ACTTCAGATAGCCAAAGTACTACAGGAAACAAATGTTGAGAACGAGCTCTGATAAAG 960  
DB 901 ACTTCAGATAGCCAAAGTACTACAGGAAACAAATGTTGAGAACGAGCTCTGATAAAG 960  
QY 961 TCTTCGGGATCCGTTTTCAGATCCTGTTTGGACCGGAGGAAATTTGACATATCC 1020  
DB 961 TCTTCGGGATCCGTTTTCAGATCCTGTTTGGACCGGAGGAAATTTGACATATCC 1020  
QY 1021 AGCTGGTTGTGTACATCGGCTCAACCTCTCTACTTGGCTGCGCTGCTGCTGCTGCTGCTG 1080  
DB 1021 AGCTGGTTGTGTACATCGGCTCAACCTCTCTACTTGGCTGCGCTGCTGCTGCTGCTGCTG 1080  
QY 1081 ACTTCCTCATCGACACTTCCAGTAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140  
DB 1081 ACTTCCTCATCGACACTTCCAGTAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140  
QY 1141 AGTGTCTGACGCTGTGTGCTCAAGAAATCTACTACAGGAGAGTGGAGTCCCATG 1200  
DB 1141 AGTGTCTGACGCTGTGTGCTCAAGAAATCTACTACAGGAGAGTGGAGTCCCATG 1200  
QY 1201 TGGAGCCAAAGCCGACATTAAGTATGCTCTCTTGTGATGATGATGATGATGATGATGATG 1260  
DB 1201 TGGAGCCAAAGCCGACATTAAGTATGCTCTCTTGTGATGATGATGATGATGATGATGATG 1260  
QY 1261 TGAACACAGCTACTAGGAGAGTCTGCAAGATGTCAGGGCCAGAGAGTCCCAAAGAC 1320  
DB 1261 TGAACACAGCTACTAGGAGAGTCTGCAAGATGTCAGGGCCAGAGAGTCCCAAAGAC 1320  
QY 1321 CTGTGATGACTTTCAGAGTTTCCAGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380  
DB 1321 CTGTGATGACTTTCAGAGTTTCCAGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380  
QY 1381 TTCTTGGACACACAGAGAGATACAGTCTGTTAGAAAGAGGCGGAGTCTTACAGTCCAGG 1440  
DB 1381 TTCTTGGACACACAGAGAGATACAGTCTGTTAGAAAGAGGCGGAGTCTTACAGTCCAGG 1440  
QY 1441 ATAGCCCTCTGTGTGCGAGTGTGGAAGTGTGCTGCCATCTCAACTCCCTCCGTAGAGCCACA 1500

DB 1441 ATAGCCCTCTGTGTGCGAGTGTGGAAGTGTGCTGCCATCTCACTCCCTGAGAGCCACA 1500  
QY 1501 GTGTGCTGAGGAGCTGTGTGCTGCCGAAAGAGCGGGGCTGCTGCTGCTGCTGCTGCTGCTG 1560  
DB 1501 GTGTGCTGAGGAGCTGTGTGCTGCCGAAAGAGCGGGGCTGCTGCTGCTGCTGCTGCTGCTG 1560  
QY 1561 TGTTCAGAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620  
DB 1561 TGTTCAGAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620  
QY 1621 CTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680  
DB 1621 CTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680  
QY 1681 GTTACGCCACCTGCGGCTTCCAGGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740  
DB 1681 GTTACGCCACCTGCGGCTTCCAGGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740  
QY 1741 GTTACGCCACCTGCGGCTTCCAGGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800  
DB 1741 GTTACGCCACCTGCGGCTTCCAGGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800  
QY 1801 AGAGTCCCTTACTGAAGCAGGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1853  
DB 1801 AGAGTCCCTTACTGAAGCAGGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1853

RESULT 2  
US-08-842-079-16  
; Sequence 16, Application US/08842079  
; Patent No. 6133434  
; GENERAL INFORMATION:  
; APPLICANT: BUELL, GARY N.  
; APPLICANT: SURPRENANT, ANNMARIE  
; APPLICANT: KAWASHIMA, ERIC  
; TITLE OF INVENTION: A PURINERGIC RECEPTOR  
; FILE REFERENCE: 1430-160  
; CURRENT APPLICATION NUMBER: US/08/842,079  
; CURRENT FILING DATE: 1997-04-28  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 3540  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-08-842-079-16

Query Match 69.2%; Score 1282.4; DB 3; Length 3540;  
Best Local Similarity 81.4%; Pred. No. 0;  
Matches 1469; Conservative 13; Mismatches 323; Indels 0; Gaps 0;

QY 11 GAGGAGGCTGTCCACATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 70  
DB 106 GAGTGAAGCTGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 165  
QY 71 GAACAAGTCACTCGGATCCAGAGCATGATTTGAGGACCATTAAGTGGTCTTCCAGT 130  
DB 166 AAACAAGTCACTCGGATCCAGAGCATGATTTGAGGACCATTAAGTGGTCTTCCAGT 225  
QY 131 GATCATCTTTTCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 190  
DB 226 GACCTGCTTTTCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 285  
QY 191 GCTGTGCTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 250  
DB 286 GCGCTTATGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 345  
QY 251 CGYGAGATGAGTGTGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 310  
DB 346 CACGAGGCGGCGGCTGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 405



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; MOLECULE TYPE: CDNA
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: CONSENSUS
US-08-742-621-2

Query Match 12.8%; Score 237; DB 2; Length 1762;
Best Local Similarity 54.4%; Pred. No. 1.2e-59;
Matches 574; Conservative 5; Mismatches 440; Indels 36; Gaps 4;

QY 55 TTTTCCAGTATGAGACGACAAAGTCACTCGGATCCACGAGCATGAATATGACCACTTA 114
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 62 TGTTCGAGTACGACACGCGCGCATCTGCTCACTCCGACGCCAAGTGGGCTATGA 121

QY 115 ATGGTTCCTCCAGTATGATCTCTTCTCTAGC---TTTGCTTTGCTGTGGTGAACA 171
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 122 ACCGCGCGGTGCAACTGCTCACTCTGGCTAGCTCATCGGTGGTGTGGTGGAAA 181

QY 172 AGCTGTACACGCGAAGAGCTGTCATCACTCTGTGCACACCAAGGTGAAGGGATAG 231
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 182 AGGCTACCGAGAACTGACTCGTGTCACTCGCTAGGACCAAGGTCAAGGCGTGG 241

QY 232 CAGAGGTGAAGAGGAGATCTGCGAGATGAGTGAAGTGTGGTGCACAGTCTTTTG 291
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 242 CTGTGAACCAACTTCTAACTTGGATTCGCGATCTGGGATGTGGGATATGTGATC 301

QY 292 ACACCGCAGACTACACTTCCCTTTGCGAGGGAGTCTTCTCTGTCGATGACAACATTC 351
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 302 CAG-----CTCAGGAGGAAACTCCCTCTCTGTCATGACCACTGTA 343

QY 352 TCAAAACAGAGGCGAAGAGCAGCGGTGTGTCCCGAGTATCCACCCGACGAGCTCT 411
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 344 TCCTCACCATGAACACAGACACAGCGGCTGTGCCCGGAGATTCAGATGCGACACTGT 403

QY 412 GTTCTCTGACCGAGGTGTGAAAAGGATGATGAGCCGCGAGACCAAGAAATTCAGA 471
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 404 GTAAATCAGATGCGAGTCTACTGCGGCTCTGCGGACCCACAGACAGGAGTCTCAA 463

QY 472 CGGAAAGGTGTAGTATGAGGAAACCAAGAACTGTGAAGTCTCTGCTGGTGGC 531
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 464 CAGGCGAGTGTGAGTCTTCAACGGGTCCGTCAAGACGTGTGAGGTGGGCGCTGTG 523

QY 532 CGATCGAGGAGTGGAGAGGCGCCCGCGCTGTCTCTTGAACAGTGCAGAAACTTCA 591
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 524 CGGTGGAGGATGACACACAGCTGCCACACCTGTCTTTTAAAGGCTGCAGAAACTTCA 583

QY 592 CNGTCTCATCAAGAACATATCGACTTCCCGCGCCCAACTACACACAGAGAAATCC 651
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 584 CTCCTTTGGTAAAGACACACTCTGGTATCCCAATTAATTCACAGAGGAAATACC 643

QY 652 TGCCAGGTTTAAATCACT-----TGACTCTCCACAGACTCAGATCCAC 699
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 644 TTCCCAACATCACCACACTTACTCTCAAGTCTGCTCATTTATGATGCTAAACAGATCC 703

QY 700 AGTGTCCATTTTCCGACTAGGAGACATCTCCGAGAAACCGCGATATTTTTCAGATG 759
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 704 TCTGCCCTATTCCTGCTTGGCAAAATAGTGGAGAACGACGAGACAGTTTCCAGGACA 763

QY 760 KGGCAATTCAGGCGGGAATAATGGCATTTGAGATCTACTGGGACTCRACTTAGACGTT 819
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 764 TGGCGGTGGAGGAGGACATCATGGGCTCCAGGTCACTGGGACTGCAACTGGACAGAG 823

QY 820 GGTTCATCATCTGCGCTCCCAATACAGATTTTCCTGCGCTTGACGACAGACCCACAG 879
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 824 CGGCTCTCTCTGCTTCCCGAGTACTCTTCCGCGCGCTCGATACACGGGAGCTTGAGC 883

QY 880 TGTCTTGTACCTCGGTCAACTCTCAGATACGCGCAAGTACTCAAGGAAAAAATG--- 936
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 884 ACAACGATATCTCTGGCTACATTTTCAGGTTTCCAGTACTACAGAGACCTGGCTGCA 943

QY 937 TTGAGAACGAGACTCTGATAAAAGTCTTGGGATCCGTTTGTGACATCTCGTTTGGCA 996
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 944 ACAGACGCGACGCTCATCAAGGCTATGAGCTACGCTCGCTTCGACATCTGTGTGGGA 1003

```

Db 517 CGGTGGAGTACACACACAGTGGCCACACCTGCTTTTAAAGGCTGCAGAACTTCA 576  
QY 592 CTGTGCTCATCAAGAACAAATATCGACTTCCCGGCGCACAACTACACACAGAGAAATCC 651  
Db 577 CTCTTTGGTTAGAACACATCTGCTATCCCAATTTAATTCACAGAGAAATCC 636  
QY 652 TGGCAGGTTAAACATCACT-----TGTACCTTCCACAAAGACTCAGAACTCCAC 699  
Db 637 TTCCACATCACTCACTTACCTCAAGTCGTGCTATTTATGATGCTAAACAGATCCCT 696  
QY 700 AGTGTCCATTTTCGACTAGAGACATCTTCGAGAAACAGCGGATTAATTTTCAGATG 759  
Db 697 TCTGCCCCATATCTCGCTTGGCAAAATAGTGGAGAACGACGACACGGTTTCCAGGACA 756  
QY 760 KGCAATTCAGGCGGATATAGGCAATTCAGATCTACCTGGGACTGCAACTAGACCGTT 819  
Db 757 TGGCGGTGGAGGAGGATCATGAGGCAATCCAGTCACTGGGACTGCAACTGGACAGAG 816  
QY 820 GGTTCATCACTGCCCTCCCAATACAGTTTCCCTCGCTTGACGACAAAGACACCAAG 879  
Db 817 CGGCTCCCTCTGCTTGGCCAGGTACTCTCTTCGCGGCTCGATACAGGAGCTTGAGC 876  
QY 880 TGTCTCTGTACCTGGCTACAACTTCAGATACGCCAAGTACTACAGGAAACAAATG--- 936  
Db 877 ACAACGTATCTCTGGCTACAAATTCAGGTTTGCCTAAGTACTACAGAGACTGGCTGGCA 936  
QY 937 TTGAGAAACGACTCTGATAAAGTCTCGGATCGGTTTTCACATCTGGTTTGGCA 996  
Db 937 ACAGAGCGGACGCTCATCAAGGCTATGGCATCGCTTGCATCATCATGTTTGGGA 996  
QY 997 CCGAGGAAAAATTTGACATTTCCAGCTGGTTGTGTACATCGCTCAACCTCTCCCTACT 1056  
Db 997 AGCAGGAAAAATTTGACATATCCCACTATGATGATGATGATGATGATGATGATGATG 1056  
QY 1057 TCGGTGCGGCTGTGTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 1091  
Db 1057 TAGGCATGGCGGCGGTGTGTGTGATGATGATGATGATGATGATGATGATGATGATG 1091

RESULT 5

US-08-750-134A-6  
; Sequence 6, Application US/08750134A  
; Patent No. 5985603  
; GENERAL INFORMATION:  
; APPLICANT: VALERA, SOLEDAD  
; APPLICANT: BUELL, GARY  
; TITLE OF INVENTION: P2X RECEPTORS (PURINOCEPTOR FAMILY)  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/750.134A  
; FILING DATE: 22-JAN-1997  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CRAWFORD, ARTHUR C.  
; REGISTRATION NUMBER: 25,327  
; REFERENCE/DOCKET NUMBER: 1430-116  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 816-4006  
; TELEFAX: (703) 816-4100  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:

; LENGTH: 1997 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-750-134A-6  
  
Query Match 12.7%; Score 234.6; DB 2; Length 1997;  
Best Local Similarity 55.5%; Pred. No. 6.8e-59;  
Matches 585; Conservative 5; Mismatches 429; Indels 36; Gaps 6;  
  
QY 55 TTTTCCAGTATGAGACGACAAAGTTCATCTGGATCCAGAGCATGAATATGGCCACCAATTA 114  
Db 135 TGTTGAGTACGACAGCGCGGCATCTGCTCATCCGACGCGTAAAGTGGGGCTCATGA 194  
QY 115 AGTGGTTCTTCACGATGATCATCTTTTCCCTAACG---TTTGCCTTCTCTGTGTAGTGA 171  
Db 195 ACCGCGGGTGCAGCTGCTCATCTCTGCTTACGTCATCGGCTGGGTGGTGTCTGTGGAAA 254  
QY 172 AGCTGTACACGCGGAAAGAGCTGTCTCATCTGTCACACCAAGCTGAGGGGATAG 231  
Db 255 AGGCTTACCAAGGAAACGGACTCCGTTGTCAGCTCGGTGACAAACCAAGGAGGTGG 314  
QY 232 CAGAGGTGAAAGAGGAGATCGTGGAGATGAGTGAAGAGTGGTGACACAGTCTCTTTG 291  
Db 315 CTGTGACCAAC-----ACCTCTCAGCTTGAATTCGGATCTGGGACGTGGCGACTAIG 368  
QY 292 ACACCGCAGATACACCTTCCCTTTGAGGGGAACTCTTTCTTCTGTGTAGTGAACAATTC 351  
Db 369 TGATTCCAG-----CTCAGGAGGAAAACTCCCTCTTCATATGACCAACATGA 416  
QY 352 TCBAACAGAGAGGCCAAGAGCAGCGGTTGTTCGAGTATCCACCCGAGGACGCTCT 411  
Db 417 TTGTCACTGTAACAGACAGACAGACAGACCTGTCCAGAGATCTCTGATAGACCAAGCATTT 476  
QY 412 GTTCTCTGACCGAGGTTGTAAGAGGATGGATGACCCGCGACAGAAAGAAATTCAGA 471  
Db 477 GTATTTCAGAGCGGACTGCTCTCTGCTGCTGGACACCCAGCAGTGGAGTTCGGA 536  
QY 472 CCGGAGGTGTGTATGTATGAGGAAACAGAGACCTGTGAAGTCTCTGCTGCTGCTGCTGCC 531  
Db 537 CTGGAAGATGTGTTCTTCAATGAGTCTGTGAAGACCTGTGAGGTGGTGTGCTGCTGCTGCC 596  
QY 532 CCATCGAGGAGTGGAGAGGCGCCCGGCTCTCTCTGTGACAGTGCCTGCTGCTGCTGCTGCTCA 591  
Db 597 CGGTGGAGAACGACTGTGGCTGCGCAAGCGCGGCTTCTTAAAGGCTGCAGAAACTTCA 656  
QY 592 CTGTGCTCATCAAGAACAAATATCGACTTCCCGCGCACAACTACACACAGAGAAACATCC 651  
Db 657 CCTCTTTGTAAGAACACATCTGTTACCCCAAGTTTAACTTCAGAGAGGAGACATCC 716  
QY 652 TGGCAGGTTTAA-----ACATCTGTGTACCTTCCCAAGACTCA---GAATCCAC 699  
Db 717 TCCCAACATCACCACTGCTCTACCTACCTAAATCTGTCATCTTACATGCTCAAAAGGATCCCT 776  
QY 700 AGTGTCCATTTTCGACTAGGAGACATCTTCGAGAGAACAGCGCATTAATTTTCAGATG 759  
Db 777 TCTGCCCATATTTCCGTCTTGGCAATTCGTTGGGAGCGGGGACATAGCTTCCAGGAGA 836  
QY 760 KGGCAATTCAGGCGGGAATATAGGCAATTCAGATCTTACTGGGACTGCAACCTAGACCGTT 819  
Db 837 TGGCAGTTGAGGAGGATCATGAGTATCCAGATCAAGTGGGACTGCACTGATGATAGAG 896  
QY 820 GGTTCATCACTGCTCTCCCAATATACAGTTTCCCTTCCGCTTGCACAGAGACCAACAG 879  
Db 897 CCGCTCTCCCTTTGCTGCCAGATATCTCTTCGCGGCTGGACACCCGAGACCTGGAC 956  
QY 880 TGTCTTGTACCTGCTTACACTTCAGATACGCCAAGTACTTACAGGA---AAACATG 936  
Db 957 ACAATGTGTCTCTGCTGCTACATTTTCAGTTTGCCTAAGTACTTACAGGACCTGCCCGCA 1016  
QY 937 TTGAGAAACGACTCTGATTAAGTCTCTGGGATCGGTTTTCACATCTGCTGCTGCTGCTGCTG 996

Db	315	CTGTGACCAAC-----ACCTCTCAGCTTGGATTCCGGATCTGSGAGCTGGCGGACTATG	368
QY	292	ACACCGGAGAGTACACTTCCCTTTGCAGGGGAACTCTTTCTTCGTGATGACAAACTTTC	351
Db	369	TGATTCCAG-----CTCAGAGGAGAAATCCCTCTTCATTATGACCACTGA	416
QY	352	TCAAACAGAGAGGCCAAGACGACGGCTTGTCGCCGAGTATCCACCGCAGGACGCTCT	411
Db	417	TTGTGTCACCGTGAACCAACACACAGACACTGTGCCAGATTTCTTGATPAGACACGACATTT	476

Db	477	GTAAATTAGAGCGGACATGCATCTCTGGCTCGTGGACACCAAGCAGTGGAGTTGGCA	536
QY	472	CCGGAAGGTGTAGTATYATGAAGGGAAACAGAAAGACCTGTGAAGTCTCTGCCTGGTGGCC	531
Db	537	CTGGAAGATGTCTCTTTCAATGAGTCTGTGAAGACCTGTGAGTGGCTGCATGCTGGCC	596
QY	532	CCATCGAGGACGTGAAGAGGCCCGCCGCTCTCTCTTTGAACAGTGCAGAAACTTCA	591
Db	597	CGTGTGAAGAACACGCTTTGGGCGTGCACACGCCGCTTTCTTAAGGCTGTCAGAAAACTTCA	656

592	CTGTGCTCATCAGACAAATATCGACTTC	CGCGGCCAACATACACCAAGAAATCC	651
QY			
657	CCCTCTTGGTAAAGAACACATCTGGTAC	CCCCAAGTTTAACTTCAGCAAGGAACATC	716
Db			
652	TGCCAGGTTTAA-----ACATCATCTGT	ACCTTCACCAAGACTCA---GAATCCAC	699
QY			
717	TCCCCACATACCAGTGCTTACCTCAAT	CGTGCAATTACAAATGCTCAAAAGGATCC	776
Db			
700	AGTGTCCATTTCGAGCTAGAGACATCTC	CGAGAACACAGGGGATAAATTTTCAGTG	759
QY			
777	TCTCCCCATTTCGTCTTGCCAAATCTG	GGGAGCGGGACATGAGTCTCCAGGAGA	836
Db			
760	KGGCAATTGAGGCGGAATTAATGGGCAT	TACAGATCTACTGGGACTGCAACTAGAC	819
QY			
837	TGGCAGTTGAGGGAGCATCATGGGTAT	CCAGATCAAGTGGGACTGCAACTGATAG	896
Db			
820	GATTCCATCACTGCCTTCCTCCAAATAC	AGTTTCCTCGCTTGACACAGACACCAAC	879
QY			
897	CCGCTCCCTTTGCCCTGCCAGATATCTC	TCCGGCGGCGCTGGACACCGGAGACTG	956
Db			
880	TGTCCTTGACTCCGTACACACTTCAGAT	ACGCCAAGTACTACAAGA--AAACAATG	936
QY			
957	ACAATGTGCTCTCTGGCTACAAATCTG	AGTTTGGCAAGTACTACAGGACCTGGC	1011
Db			
937	TTGGAACAACGGACTCTGATATAAAGTC	TCTCCGGATCCGGTTTGACATCCTGTTT	996
QY			
1017	AGAGGACGCCACACTCACCAAGGGTAC	GGCATCCGCTTTTGACATCATGTTTGG	1071
Db			
997	CCGGAGGAAAATTGTACATTAATCCAC	TATGTGTGTACATCGGCTCAACCTCTC	1056
QY			
1077	AGGCTGGGAAGTTTGACATCATCCCAT	GATGATCAACGTTGGCTCTGGCTGGCG	1136
Db			

DB 1137 TCGGGGTGGGACGGTGCTCTGTGACGTATAGTC 1171

RESULT 7  
US-08-750-134A-10  
; Sequence 10, Application US/08750134A  
; Patent No. 5985603  
; GENERAL INFORMATION:  
; APPLICANT: VALSEA, SOLEDA  
; APPLICANT: BUELL, GARY  
; TITLE OF INVENTION: P2X RECEPTORS (PURINOCEPTOR FAMILY)  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA

```

; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,134A
; FILING DATE: 22-JAN-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAWFORD, ARTHUR C.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 1430-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4006
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2643 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-750-134A-10

Query Match 11.0%; Score 203.8; DB 2: Length 2643;
Best Local Similarity 54.8%; Pred. No. 9.4e-50;
Matches 447; Conservative 5; Mismatches 342; Indels 21; Gaps 2;

QY 285 GTCCTTTGACACCGCAGACTACACTTCCCTTTTCAGGGGAACTCTTCTTCGTGATGACA 344
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 423 GTCCTGGAGTGTGGCTGACTAGCTTCTCCAGCCAGGGGGGAGACACTCTTCGTGTCATG 482
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 345 AACTTCTCAAAACAGAGAGCCAGAGACGGGTGTCTCCGAGTATCCCAACCGCAGG 404
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 483 ACCAATTTCATCGTGACCCCGAAGCAGACTCAAGGCTACTGCGCAGAGCACCCAGAGGG 542
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 405 ACGCTGTGTCTCTGACCGAGGTTGTAAAAAGGATGGATGGACCGCAGAGCAAGAGA 464
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 543 GGCATATCAAGAGACAGAGTGGCTGTACCCCTGGGAAGGCCAGAGGAGGCCAAGGC 602
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 465 ATTCAAGCGGAGGTGTGTAGTATATGAAGGAAACAGAACCTGTGAAGTCTCTGCC 524
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 603 ATCCGACGGCAAGTGTGTGGCTTCAACGACACTGTGAAGACGTTGTGAGATCTTTGGC 662
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 525 TGGTGGCCCATCGAGGACGTGGAGAGGCCCCCGGCTGCTCTTTGAACAGTCCCGAA 584
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 663 TGGTGGCCCGTGGAGGTGGATGACGACATCCCGCGCCCTGCGCTTCTCCGAGAGCCGAG 722
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 585 AACTTCACTGTGTCATCAAGAACATATGACTTCCCGGCCAACACTACACCACGAGA 644
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 723 AACTTCACTCTTTTCATCAAGACAGCATCAGTTTCCACGCTTCAAGTCAACAGCGCC 782
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 645 AACATCGTCCAGGTTTAAA-----CATCACTTGTACTTTCCACAAAGACTCAG 692
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 783 AACCTGTGTGGAGGAGTGAATGTGCCCATGAAGACCTGCCCTTTTTCAGAGACCCCTG 842
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 693 AATCCACAGTGTCCATTTTCCGACTAGGAGACATCTTCCGAGAAACAGCGCATATTTT 752
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 843 CAOCCCGTGTGCCAGTCTTCCAGCTTGGCTACGTGGTGAAGAGTCAAGCCAGCAACTTC 902
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 753 TCAGATGKGCAATTCCGGCGGGAATAATGGCACTTGATCTACTGGGACTGCAACTCA 812
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 903 AGCACTTGGCTGAGAGAGGTGGAGTGGTTGGCTACCCCTGACTGGCACTGTGACCTG 962
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 813 GACCGTGTGTTCCATCACTGCGCTCCCAATAACAGATTTTCCTGCGCTTGACGACAGACC 872
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 963 GACTGGCAGCTAGGCACTGCAGACCACTATGAGTTCCATGGCTGTACGAGAGAA 1022
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 873 ACCAAGCTGTCTTGTACCTGGGCTACAACCTTCAGATACGCCAAGTACTAAGGAAC 932
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 543 GGCATATGCAAGAGAGACAGTGGCTGTACCCCTGGGAAAGGCCCAAGAGGCCCAAGC 602  
QY 465 ATTACAGCGGAGAGTGTAGTATGAGAGGAAACAGACCTGTGAGTCTGTCC 524  
Db 603 ATCCGACGGGCAAGTGTGGCTTCAAGACACTGTGAAGAGTGTGAGATCTTTGGC 662  
QY 525 TGGTGGCCATCGAGGAGTGTGAAGAGGCCGCCGCTGTCTTCTTGAACAGTGCAGAA 584  
Db 663 TGGTGGCCGAGAGTGTGAGAGCAATCCCGGCTGTCCCTTCTCCAGAGGCCGAG 722  
QY 585 AACTTCACTGTCTCATCAAGACAATATGAGTCTCCCGGCAACAACTACACAGAGA 644  
Db 723 AACTTCACTTCTTTCATCAAGACAGCATCAGCTTCCAGGCTTCAAGGTCAACAGGCG 782  
QY 645 AACATCTCCAGGTTTAAA-----CATCACTTGTACTTCCACAGACTCAG 692  
Db 783 AACTTGGAGAGGTGAATGTGCCCATGAGACCTGCTCTTTCACAGACCTTG 842  
QY 693 AATCCACAGTGTCCCATTTTCCGACTAGGAGACATCTCCGAGAAACAGGCGGATAATTT 752  
Db 843 CACCCCTGTGCCAGTCTTCCAGCTGGCTAGGTGGTGCAGAGTCAAGGCGAGACTTC 902  
QY 753 TCAGATGKGCAATTCAGGCGGAATATGAGGCAATGAGATCTACTGGGACTCAACCTA 812  
Db 903 AGCACCTCGGCTGAGAGAGGTGGAGTGGTGGCATCACCATCGACTGGCACTGTGACCTG 962  
QY 813 GACCGTGTGTCCATCACTGCGRCCCAATACAGTTCCTCGCTTGGAGCAGAGACC 872  
Db 963 GACTGCGAGTACGCACTGACACCATCTATGAGTTCATGGCTGTACGAGAGAAA 1022  
QY 873 ACCAAGTGTCTTGTACCTGGCTCAACTTCAGATAGCGCAAGTACTACAAGAGAAAC 932  
Db 1023 A-----ATCTCTCCAGGCTTCAACTTCAGTGTGCCAGGCACTTTTGGAGAC 1073  
QY 933 AATGTTGAGAAAGGACTCTGATFAAAGTCTTCGGGATCCGTTTGTACATCTGGTTTT 992  
Db 1074 GGAACCAACTACCGCTCACTCTTCAAGGTGTGGGATTCGTTTGTACATCTCGTGGAC 1133  
QY 993 GGCACCGGAGGAAATTTGACATTCACAGTGTGTGTGATCATCGCTCAACCCCTCC 1052  
Db 1134 GCAAGCGGGAAGTTTGAATCATCCCTACAAATGACACCATCGGCTCTGGAATGGC 1193  
QY 1053 TACTTGGTCTGGGCTGT 1087  
Db 1194 ATCTTTGGGTGGCCACAGTCTCTGTGACCTGCT 1228

## RESULT 9

US-08-750-134A-4

Sequence 4, Application US/08750134A

Patent No. 5985603

GENERAL INFORMATION:

APPLICANT: VALERA, SOLEDAD

APPLICANT: BUELL, GARY

TITLE OF INVENTION: P2X RECEPTORS (PURINOCEPTOR FAMILY)

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON &amp; VANDERHYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/750,134A

FILING DATE: 22-JAN-1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: CRAWFORD, ARTHUR C.  
REGISTRATION NUMBER: 25,327  
REFERENCE/DOCKET NUMBER: 1430-116  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4006  
TELEFAX: (703) 816-4100  
INFORMATION FOR SEQ. ID NO. 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1837 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
IMMEDIATE SOURCE:  
CLONE: rat P2x from vas deferens  
US-08-750-134A-4

Query Match 8.6%; Score 159.6; DB 2; Length 1837;  
Best Local Similarity 50.7%; Pred. No. 7.8e-37;  
Matches 434; Conservative 6; Mismatches 395; Indels 21; Gaps 2;

QY 244 AGGAGATCGYGGAGATGGAGTGAAGAAGTGTGTGCACAGTGTCTTTTGACACCGCAGACT 303  
Db 418 AGGCTTGGCTGTGACCCAGCTCCAGGGCTGGACCCAGCTCTGGGAGCTGGCTGACT 477  
QY 304 ACACCTTCCCTTTGAGGGGNACTCTTCTTCTGTGATGACAAACTTTCTCAAAACAGAG 363  
Db 478 ATCTCTCCACAGACAGGGGAGAGCTCTCTTTAGTTATGACCAACTTCATCGTGAACC 537  
QY 364 GCCAAGAGCAGCGGTGTGTCCCGAGTATCCACCGCAGGAGCCTCTGTCTCTGACC 423  
Db 538 CTCAGCAGACTCAAGGCCATGTGCGAGAACCCAGAGGTGGCATATGCCAGGATGACA 597  
QY 424 GAGTTGTHAAAGGGATGATGACCCCGCAGAGAAAGTAATTCAGACGGAGGTGG 483  
Db 598 GTGGCTGCACTCCAGGAAAGGAGAAAGGAAAGCCAAAGTATTGCGACAGCAACTGTG 657  
QY 484 TAGTATGAGGGAGAACACAGAGACCTGTGAAGTCTCTGCTGTGTGCCCATCGAGGCGAG 543  
Db 658 TGGCTTCAATGGCACTGTGAGACATGTGAGATCTTTGGTGTCTGTGAGAGTGG 717  
QY 544 TGAAGAGAGCCCGCGCTGTCTTGAACAGTGCAGGAAACTTCATCTGTCTCATCA 603  
Db 718 ATGACAAGATCCAGCCCTGCTCTTCTGCTGAGCTGAGACTTCACCCCTCTTCATCA 777  
QY 604 AGAACAATATCAGTTCGCCGCGCCCACTACACACAGAGAAACATCCTGCCAGGTTAA 663  
Db 778 AAAACAGCATCAGCTTCCAGGCTTCAAGGTCAACAGGCGCAACCTGTGAGAGGAGTGA 837  
QY 664 ACATCACTTGTA-----CCTTCCACAAGACTCAGAAATCCACAGTGTCCCATTT 711  
Db 838 ACGGCACTTACATGAAGTGGCTCTATCAACAGATTCAACACCCCTGTGCCAGTCT 897  
QY 712 TCCGACTAGGAGACATCTCCGAGAAACAGGCGGATAATTTTCAGATGKGCAATTCAGG 771  
Db 898 TCAACCTTGGCTATGTGTGCGAGAGTCAGGCCAGGACTTCCGAGCAGCTTGTGTGAGAAG 957  
QY 772 GCGAATAATGGCATTCAGATCTACTTGGGACTGCAACTAGACCTGAGTGTGTCTCACT 831  
Db 958 GTGGGTGGTGGTATCACCATTGACTGGAAGTGTGATCTGGACTGGCAGTTCGGCACT 1017  
QY 832 GCCTCCCAATACAGATTTCCCTGCGCTGAGCAGCAAGACCAACCAAGCTGCTCTGTACC 891  
Db 1018 GCAACCCATCTACAGTTCACAGTTCACCGGACTATGAGGAGAGAAC-----TGTCTC 1068  
QY 892 CTGGCTTACAACTTCAGATAGCCCAAGTACTACAAGAAACAAATGTTGAGAAACGAGTCT 951  
Db 1069 CAGGCTTCAACTTCAGATTTGCCAGGCAATTCGTGTCAGATGAGGAGAACCCGCTGCTACC 1128  
QY 952 TGATAAAGTCTGCGGATCCGTTTGTGACATCTCTGGTTTGGCAGCGGAGAAATTTG 1011  
Db 1129 TCTTCAAGGTGTTGGGATTCACATCTTGTGATGATCTTGTGATGCGCAGGCTGGGAGTTG 1188







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/ ADDRESSEE: NIXON & VANDERHYE P.C.
/ STREET: 1100 NORTH GLEBE ROAD
/ CITY: ARLINGTON
/ STATE: VIRGINIA
/ COUNTRY: U.S.A.
/ ZIP: 22201-4714
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/750,134A
/ FILING DATE: 22-JAN-1997
/ CLASSIFICATION: 536
/ ATTORNEY/AGENT INFORMATION:
/ NAME: CRAWFORD, ARTHUR C.
/ REGISTRATION NUMBER: 25,327
/ REFERENCE/DOCKET NUMBER: 1430-116
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 816-4006
/ TELEFAX: (703) 816-4100
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cdna
/ US-08-750-134A-8

Query Match      7.6%; Score 140.2; DB 2; Length 1753;
Best Local Similarity 52.6%; Pred. No. 3.9e-31;
Matches 457; Conservative 3; Mismatches 376; Indels 33; Gaps 6;

QY 254 GGAGATGGAGTGAAGTGGTGCACAGTGTCTTTGACACCGCAGACTACACTTCCC 313
DB 351 GGTGAAGGCTTCGGCGCTATGCCAACAGACTCATGCGTGTGGATTATGACCCC 410
QY 314 TTTCAGGGAACCTCTTTCT---TCGTGATGACAACTTTCTCAAAACAGAGCCCAAGA 370
DB 411 ACCCCAGGCGACCTGTCTTTGTCTATCATCAACCAATGATGTTTACTGAAATCAAT 470
QY 371 GCACGGTGTGTCGCGGAGTATCCACCCGCGAGACCTCTGTCTCTGACCGAGGTG 430
DB 471 GCAAGGATTCGTCCAGAAAT---GAAGAGAAATACCGCTGTGTCTGTGACAGCCAGTG 527
QY 431 TAAAAGGATGGATGACCGCGAGCAAAAGAAATTCAGACCGGAAGTGTGTAGTRYA 490
DB 528 TGGGCTGACG-----CTTCCAGTGGGGGATCCTCACCGCGCGTGGTGACCTA 581
QY 491 TGAAGGGAACAGAAAGACCTGTGAAGTCTCTGCTGTCGCCATCGAGCGAGTGAAGA 550
DB 582 CAGCTCTGTTCTCGGACCTGTGAGATCCAGGGCTGTGTGCCCA-----CTGAGGTGA 635
QY 551 GSCCCCGGCGTCTCTCTGACACAGTGGCGAAATTCACCTGTCTCTCATCAGAACAA 610
DB 636 CACCGTGGAGATGCTATCATGATGGAGCTGAGAACTTCACCATTTTCATCAAGAACAG 695
QY 611 TATGACTTCCCGGCGCAACTACACCCAGCAAAATCCTCCAGGTTTAAACATCAC 670
DB 696 CATCGTTTCCCTCTCTCACTTTGAGAGGGAAATCCTCCCTAACTCAACGACAA 755
QY 671 T-----TGTACCTTCCACAAGACTCAGAAATCCACAGTGTCCCATTTTCCGACT 718
DB 756 GGACATAAGAGGTGCGCTTCCACCTCAAAAGGCCCATTTTGGCCCATCTCAGGGT 815
QY 719 AGGAGACATCTCCGGAACAGCGGATATTTTCAGATGKGGAATTCAGGCGGGAAT 778
DB 816 AGGGATGTGGTAAAGTTGCTGGACAGAGATTTTGCAAGCTGGCCCGCAGCGGTGGGT 875
QY 779 ATGGGCAATTCAGATCTACTGGGACTGCAACTAGACCGTGTGGTTCCACTGCTCC 838

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876 TCTGGTATTAGATCGGCTGGTGGTATCGGATCTAGACAAGGCTGGGACCACTGCATCCC 935
839 CAATACAGTTTCCTCGCTTTCAGCAGAACACCAACAGTGTCTCTGTTACCTGGCTA 898
936 TAAATATTCTCTACTCGGCTGGATGGATTTCTGAGAAAAGCAGTGTTCCTCCCTGGCTA 995
899 CACTTCAGATAGCCCAAGTACTACAA--GGAACAATGTTGAGAACGAGCTCTGAT 955
996 CACTTCAGGTTTGGCAATACTATAAGATGGAGAAGCGCAGGATACCGCACTCTCT 1055
956 AAAAGTCTTCGGATCCGTTTTCACATCCTGTTTGGCACCGGAGGAAATTTGACAT 1015
1056 GAGGCTTTGGATCCGCTTTGATGTCTGATATATGGAACGCTGGAAGTCAACAT 1115
1016 TATCCAGCTGTGTGTATCATCGGCTCAACCTCTCTCTACTTCTGCTCGGCTCGGCTGT 1075
1116 CATCCCACTTATCATGCTGCTGCGGCTCTCACTTCTGTGGAGTGGGAGTGGCTTCT 1175
1076 CATGCACTTCTCATCGACASTTACTCCA 1104
1176 CTGTGACATCATCTGCTCAATTTCTCTCA 1204

RESULT 14
US-09-363-745-8
; Sequence 8, Application US/09363745
; Patent No. 6194162
; GENERAL INFORMATION:
; APPLICANT: VALERA, SOLEDAD
; TITLE OF INVENTION: P2X RECEPTORS (PURINOCEPTOR FAMILY)
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/363,745
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/750,134
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAWFORD, ARTHUR C.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 1430-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4006
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1753 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-09-363-745-8

Query Match      7.6%; Score 140.2; DB 4; Length 1753;
Best Local Similarity 52.6%; Pred. No. 3.9e-31;
Matches 457; Conservative 3; Mismatches 376; Indels 33; Gaps 6;

QY 254 GGAGATGGAGTGAAGTGGTGCACAGTGTCTTTGACACCGCAGACTACACTTCCC 313
DB 351 GGTGAAGGCTTCGGCGCTATGCCAACAGACTCATGCGTGTGGATTATGACCCC 410
QY 314 TTTCAGGGAACCTCTTTCT---TCGTGATGACAACTTTCTCAAAACAGAGCCCAAGA 370
DB 411 ACCCCAGGCGACCTGTCTTTGTCTATCATCAACCAATGATGTTTACTGAAATCAAT 470
QY 371 GCACGGTGTGTCGCGGAGTATCCACCCGCGAGACCTCTGTCTCTGACCGAGGTG 430
DB 471 GCAAGGATTCGTCCAGAAAT---GAAGAGAAATACCGCTGTGTCTGTGACAGCCAGTG 527
QY 431 TAAAAGGATGGATGACCGCGAGCAAAAGAAATTCAGACCGGAAGTGTGTAGTRYA 490
DB 528 TGGGCTGACG-----CTTCCAGTGGGGGATCCTCACCGCGCGTGGTGACCTA 581
QY 491 TGAAGGGAACAGAAAGACCTGTGAAGTCTCTGCTGTCGCCATCGAGCGAGTGAAGA 550
DB 582 CAGCTCTGTTCTCGGACCTGTGAGATCCAGGGCTGTGTGCCCA-----CTGAGGTGA 635
QY 551 GSCCCCGGCGTCTCTCTGACACAGTGGCGAAATTCACCTGTCTCTCATCAGAACAA 610
DB 636 CACCGTGGAGATGCTATCATGATGGAGCTGAGAACTTCACCATTTTCATCAAGAACAG 695
QY 611 TATGACTTCCCGGCGCAACTACACCCAGCAAAATCCTCCAGGTTTAAACATCAC 670
DB 696 CATCGTTTCCCTCTCTCACTTTGAGAGGGAAATCCTCCCTAACTCAACGACAA 755
QY 671 T-----TGTACCTTCCACAAGACTCAGAAATCCACAGTGTCCCATTTTCCGACT 718
DB 756 GGACATAAGAGGTGCGCTTCCACCTCAAAAGGCCCATTTTGGCCCATCTCAGGGT 815
QY 719 AGGAGACATCTCCGGAACAGCGGATATTTTCAGATGKGGAATTCAGGCGGGAAT 778
DB 816 AGGGATGTGGTAAAGTTGCTGGACAGAGATTTTGCAAGCTGGCCCGCAGCGGTGGGT 875
QY 779 ATGGGCAATTCAGATCTACTGGGACTGCAACTAGACCGTGTGGTTCCACTGCTCC 838

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Result No.	Query %			ID	Description
	Score	Match	Length		
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2	1837.8	99.2	2164	15	US-10-475-523-191
3	237.	12.8	1389	11	US-09-833-082-1
4	203.8	11.0	2633	11	US-09-969-347-225
5	147.4	8.0	4900	12	US-09-977-221-1
6	142.6	7.7	11270	12	US-09-977-221-3
7	113.6	6.1	515	12	US-09-918-995-31290
8	102.6	5.5	1956	11	US-09-864-864-331
9	94.6	5.1	423	11	US-09-864-864-254
10	90.8	4.9	276	11	US-09-960-352-11220
11	89.8	4.8	678	15	US-10-027-632-103774
12	89.8	4.8	698	15	US-10-027-632-103775
13	57.2	3.1	488	12	US-09-918-995-5305
14	52.8	2.8	229	11	US-09-998-598-1742
15	51.2	2.8	941	15	US-09-764-847-250
16	51.2	2.8	941	15	US-10-092-154-250
					Sequence 2, Appli
					Sequence 191, App
					Sequence 1, Appli
					Sequence 225, App
					Sequence 1, Appli
					Sequence 3, Appli
					Sequence 31290, A
					Sequence 331, App
					Sequence 254, App
					Sequence 11220, A
					Sequence 103774,
					Sequence 103775,
					Sequence 5505, Ap
					Sequence 1742, Ap
					Sequence 250, App
					Sequence 250, App



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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-175-523-191

Query Match          99.2%; Score 1837.8; DB 15; Length 2164;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1830; Conservative 16; Mismatches 3; Indels 0; Gaps 0;

QY 5 CGCAGGAGGAGGCTGTCACCATGCGCGCCCTGCTGCAGCTGCATGATGTTTCCAGTA 64
Db 57 CGCAGGAGGAGGAGGCTGTCACCATGCGCGCCCTGCTGCAGCTGCATGATGTTTCCAGTA 116
QY 65 TGAGACGAACAAAGTCACATCGGATCCAGAGCATGAATATGACCACTTATGATGTTCT 124
Db 117 TGAGACGAACAAAGTCACATCGGATCCAGAGCATGAATATGACCACTTATGATGTTCT 176
QY 125 CCACGTGATCATCTTTTCTACGTTTGTCTGCTGCTGAGTGACAAAGCTGTACCAAGCG 184
Db 177 CCACGTGATCATCTTTTCTACGTTTGTCTGCTGCTGAGTGACAAAGCTGTACCAAGCG 236
QY 185 GAAAGAGCCTGTATCAGTTCTGTGCACACCAAGGTGAAGGGATAGCAGAGGTGAAGA 244
Db 237 GAAAGAGCCTGTATCAGTTCTGTGCACACCAAGGTGAAGGGATAGCAGAGGTGAAGA 296
QY 245 GGAGATCGYGGAATGGAGTGAAGAAGTTGGTGACAGTGTCTTTTGACACCGCAGACTA 304
Db 297 GGAGATCGTGGAATGGAGTGAAGAAGTTGGTGACAGTGTCTTTTGACACCGCAGACTA 356
QY 305 CACCTTCCCTTTCAGGGGAACTCTTTCTTCGTGATGACAAACTTTTCAAAAACAGAAG 364
Db 357 CACCTTCCCTTTCAGGGGAACTCTTTCTTCGTGATGACAAACTTTTCAAAAACAGAAG 416
QY 365 CCAAGACACGCGTTGTGTCAGTATCCACCCAGGAGCGTCTGTTCTCTGACCG 424
Db 417 CCAAGACACGCGTTGTGTCAGTATCCACCCAGGAGCGTCTGTTCTCTGACCG 476
QY 425 AGGTTGTAAGGAGGATGATGGACCCAGACAGAAAGAAATTCAGACCGGAAGGTGT 484
Db 477 AGGTTGTAAGGAGGATGATGGACCCAGACAGAAAGAAATTCAGACCGGAAGGTGT 536
QY 485 AGTYATGAAGGAACCAAGAACCTGTGAAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 544
Db 537 AGTGCATGAAGGAACCAAGAACCTGTGAAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 596
QY 545 GGAAGAGGCCCCCGGCTGCTCTTGAACAGTGGCGGAAGAACTCACTGTGCTATCAA 604
Db 597 GGAAGAGGCCCCCGGCTGCTCTTGAACAGTGGCGGAAGAACTCACTGTGCTATCAA 656
QY 605 GAAACAATATCGATCTCCCGGCCACACTACACACGAGAAACATCTCTCCAGGTTTAA 664
Db 657 GAAACAATATCGATCTCCCGGCCACACTACACACGAGAAACATCTCTCCAGGTTTAA 716
QY 665 CATCACTGTACCTTCCACAGACTCAGAAATCCACAGTGTCCCATTTTCCAGCTAGAGA 724
Db 717 CATCACTGTACCTTCCACAGACTCAGAAATCCACAGTGTCCCATTTTCCAGCTAGAGA 776
QY 725 CATCTTCGGAACAAAGGCGATAATTTTCAGATGKGCAATTCAGGGCGGAATAATGGG 784
Db 777 CATCTTCGGAACAAAGGCGATAATTTTCAGATGKGCAATTCAGGGCGGAATAATGGG 836
QY 785 CATTGAGATCTATGGAATGCAACCTAGACCGTTGGTTTCCATCACTGCCCTCCCAATA 844
Db 837 CATTGAGATCTATGGAATGCAACCTAGACCGTTGGTTTCCATCACTGCCCTCCCAATA 896
QY 845 CAGTTTCCTTCGCTTTCAGACAGAACACCAACAGCTGCTGTTGCTACCTTCGCTACACT 904
Db 897 CAGTTTCCTTCGCTTTCAGACAGAACACCAACAGCTGCTGTTGCTACCTTCGCTACACT 956
QY 905 CAGATACGCCAAGTACTACAGGAAACAAATGTTGAAAGAGGACTCTGTAAGAAAGCTT 964
Db 957 CAGATACGCCAAGTACTACAGGAAACAAATGTTGAAAGAGGACTCTGTAAGAAAGCTT 1016
QY 965 CGGGATCCGTTTGACATCCTGTTTGGCACCAGGAGGAAATTTGACATTATCCAGCT 1024
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Db 1017 CGGGATCCGTTTGGACATCTCGTTTGGCACCGGAGGAAATTTGACATTATCCAGCT 1076
QY 1025 GGTGTGTACATCGGCTCAACCCCTCTCTACTTCTGGCTGCGCCTGTGTGTATCCAGCT 1084
Db 1077 GGTGTGTACATCGGCTCAACCCCTCTCTACTTCTGGCTGCGCCTGTGTGTATCCAGCT 1136
QY 1085 CCTCATCGCACTTACTTCCAGTAAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1144
Db 1137 CCTCATCGCACTTACTTCCAGTAAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1196
QY 1145 CTGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1204
Db 1197 CTGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1256
QY 1205 GCCAAAGCGGACATTAAGTATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1264
Db 1257 GCCAAAGCGGACATTAAGTATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1316
QY 1265 CCACGACCTACTAGGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1324
Db 1317 CCACGACCTACTAGGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1376
QY 1325 GATGAGCTTACAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1384
Db 1377 GATGAGCTTACAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1436
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Db 1437 TGGACACACAGAGAGATACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1496
QY 1445 CCCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1504
Db 1497 CCCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1556
QY 1505 CCTGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1564
Db 1557 CCTGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1616
QY 1565 CAGGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1624
Db 1617 CAGGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1676
QY 1625 GCTGCGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1684
Db 1677 GCTGCGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1736
QY 1685 GCGCACCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1744
Db 1737 GCGCACCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1796
QY 1745 CCGCTGGAGATCCGGAAGAGTTTCCAAAGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1804
Db 1797 CCGCTGGAGATCCGGAAGAGTTTCCAAAGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1856
QY 1805 TCCTTACTGAAGCAGGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1853
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RESULT 3
US-09-833-082-1
; Sequence 1. Application us/09833082
; Patent No. US20020151480A1
; GENERAL INFORMATION:
; APPLICANT: Chum, Miyoung
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 10218
; FILE REFERENCE: MNI-227
; CURRENT APPLICATION NUMBER: US/09/833,082
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 1
; LENGTH: 1389
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-833-082-1

Query Match      12.8%; Score 237; DB 11; Length 1389;
Best Local Similarity 54.48; Pred. No. 4.8e-64;
Matches 574; Conservative 5; Mismatches 440; Indels 36; Gaps 4;

QY 55 TTTCCAGTATGAGACGAAAGAAAGTCACTCGGATCCAGAGCATGAATTAATGACACATTA 114
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 62 TGTTCAGTATGAGACGACGCGCGCATCGTGTCTATCCGACGCGCAAGTGGGCTCATGA 121
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 115 AGTGGTCTTCAGCTGATCATCTTTTCTACG---YTTGCTTTGCTGTGGTGAAGACA 171
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 122 ACCGGCGGTGCAACTCTCATCTGGCTACGTACGTGGTGGTGGTGGTGGTGGTGGTGG 181
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 172 AGCTGTACACGCGAAAGACCTGTCTATCAGTCTGTGCACACCAAGGTGAAGGGATAG 231
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 182 AGGCTACACGAAGACTGACTCGTGTGCTAGCTCGGTACACCAAGGTCAAGGGCGTGG 241
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 232 CAGAGGTGAAGAGAGAGATCGYGGAGATGGAAGTGAAGAGTGGTGCACAGTGTCTTTG 291
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Db 242 CTGTGACCAACACTCTTAACCTTGGATTCCGGATCCGGATGCGGATTTATGTATAC 301
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QY 292 ACACCGCAGATACACCTTCCCTTCAGGGGAACCTCTTCTTCGTGATGACAAACTTTC 351
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QY 352 TCAAAACAGAGGCGCAAGACGAGCGGTGTGTCCCGAGTATCCACCCGACGAGCGTCT 411
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QY 412 GTTCTCTGACCGAGTGTGAAGAAGGATGATGAGACCCGACAGCAAGAAATTCAGA 471
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QY 472 CCGGAGGTGTGTAGTATGAAGGAACACAGAGACTGTGAAGTCTCTGCTCTGCTGCC 531
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Db 464 CAGGAGGTGTGTAGTCTTAACGGGTCTGTCAGACGTGTGAGGTGGCGGCTGTGCTGCC 523
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QY 532 CCATCGAGCAGTGAAGAGGCCCCCGGCTCTCTCTTTGAACAGTGCAGCCGAAAACTTCA 591
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 524 CGGTGGAGGATGACACACAGTCCCAACCTGCTTTTAAAGGCTGCAGAAACTTCA 583
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QY 592 CTGTGCTATCAGAACATATCGACTTCCCGGCGCACACTACACACAGAGAAATCC 651
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 584 CTCTTTTGGTTAAGAACACATCTGGTATCCCAAAATTTAATTTACAGAAAGGAATATCC 643
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 652 TGCAGGTTTAAACATCACT-----TGTACCTTCCACAGACTCAGAATCCAC 699
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 644 TTCCCAACATCAACACTACTACCTCACTGCTGCTTTATGATGCTAAGACAGATCCCT 703
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 700 AGTGTCCCATTTTCGACTAGAGACATCTTCCGAGAAACAGCGCATATTTTCAGATG 759
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 704 TCTGCCCCATATTCGCTTGGCAAAATAGTGGAGACGCGAGGACAGATTTCCAGGACA 763
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 760 KGCATATCAGGGGGAATATGGCATTGAGATCTCTGAGTCTGCACTTACCTAGACCGT 819
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 764 TGGCCGTGGAGGAGGATATGGGATCCAGGTCACTGGGACTGCAACCTGGACAGAG 823
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 820 GGTTCATCACTGCCCTCCCAATATAGTTTCCRTCGCTTGGAGACAGACCAACACG 879
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 824 CCGCTTCCCTCTGCTTCCAGGTACTCTTCCGCGGCTCGATACAGGGAGTGTGAGC 883
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 880 TGTCTTTGACCTTGGCTTACACTCTCAGATACGCCAAGTACTACAGAGAAACAATG--- 936
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 884 ACACGATATCTCTGCTTACAATTTACAGGTTTGGCAAGTACTACAGAGACCTGGCTGGCA 943
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 937 TTGAGAAAGGACTCTGATAAAGTCTTGGGATCCGTTTTCATCTCTGTTTGGCA 996
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 944 ACAGAGCGGCACGCTCATCAGGSCCTATGSCATCCGCTTCGACATCATTTGTTGGGA 1003
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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OTHER INFORMATION: Clone ID: 48-LIB3058-028-Q1-K1-D8  
US-09-960-352-11220

; sequence 103775, Application US/I002/632  
; GENERAL INFORMATION:

APPLICANT: WANG, DAVID G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; TITLE OF INVENTION: Polymorphisms in the Human Genome  
 ; FILE REFERENCE: 108827.129

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; CURRENT APPLICATION NUMBER: US/10/027,632
;
; CURRENT FILING DATE: 2002-04-30

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; PRIOR APPLICATION NUMBER: US 60/218,006  
 : PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676  
: PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483  
 ; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR APPLICATION NUMBER: US 60/146,002

; NUMBER OF SEQ ID NOS: 325720

; SEQ ID NO 103775

LENGTH: 0.50  
TYPE: DNA

US-10-027-632-103775

Query Match	4.8%	Score 89.8
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Best Local Similarity 96.8%; Pred. No. 1  
Matches 92: Conservative 0: Mismatch

1759 GGAAAGAGTTTC CRAAGAGTGAAGGCAGT

D<sub>b</sub> 1 GGAAAGAGTTTCBAAAGAGTGAAGGGCACT

07  
1819 : 2000

61  
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

RESULT 13  
HS-00-018-005-5505

; Sequence 5505, Application US/09918995

; GENERAL INFORMATION:

; TITLE OF INVENTION: NOVEL NUCLEIC ACID SE

FILE REFERENCE: 20411-756

CONCURRENT APPLICATION NUMBER: 05/09/510/333  
CURRENT FILING DATE: 2001-07-30

;; PRIOR APPLICATION NUMBER: US/09/233,076  
;; PRIOR FILING DATE: 1999-01-20

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; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0

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; SEQ ID NO 5505
; LENGTH: 458

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; TYPE: DNA
; ORGANISM: Homo sapiens

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DS-09-918-995-5505



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 18, 2003, 16:29:01 ; Search time 2708 Seconds  
(without alignments)  
11082.067 Million cell updates/sec

Title: US-09-977-221-2  
Perfect score: 1853  
Sequence: 1 aaacgcaggaggaggct.....cgtgttaatccacacattt 1853

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em.estba:\*

2: em.esthum:\*

3: em.estin:\*

4: em.estmu:\*

5: em.estov:\*

6: em.estpl:\*

7: em.estro:\*

8: em.htc:\*

9: gb.estl:\*

10: gb.est2:\*

11: gb.htc:\*

12: gb.est3:\*

13: gb.est4:\*

14: gb.est5:\*

15: em.estfun:\*

16: em.estom:\*

17: gb.gss:\*

18: em.gss\_hum:\*

19: em.gss\_inv:\*

20: em.gss\_pln:\*

21: em.gss\_vit:\*

22: em.gss\_fun:\*

23: em.gss\_mam:\*

24: em.gss\_mus:\*

25: em.gss\_other:\*

26: em.gss\_pro:\*

27: em.gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	1634.6	88.2	3013	11	BC007679	Homo sapi	BC007679 Homo sapi
2	675.2	36.4	795	13	BI861622		BI861622 603350486
3	671.8	36.3	946	12	BF347747		BF347747 602022588
4	666.8	36.0	937	12	BF768165		BF768165 602744202
5	645.4	34.8	932	13	BI603534		BI603534 603244436
6	619.8	33.4	769	12	BG766449		BG766449 602739207

7	564	30.4	860	13	BI598073		BI598073 603252308
8	553.8	29.9	841	12	BG769595		BG769595 602744503
9	547.4	29.5	808	12	BF689446		BF689446 602186810
10	498.6	26.9	817	10	BE382829		BE382829 601297884
c	487.6	26.3	1022	12	BF690388		BF690388 602186810
11	487.6	26.3	1022	12	BF690388		BF690388 602186810
12	430	23.2	543	12	BF347290		BF347290 602021043
13	400.8	21.6	642	14	BQ554327		BQ554327 H4027E01-
14	390.2	21.1	783	12	BF769470		BF769470 602742429
15	373	20.1	555	12	BF347097		BF347097 602020852
16	288.6	15.6	475	10	BE689531		BE689531 uw55f09.y
17	246.2	13.3	247	9	AA210664		AA210664 PMV0056 K
18	237	12.8	1844	11	BC017458		BC017458 Homo sapi
19	235.6	12.7	368	10	BE448796		BE448796 ut83h11.y
20	225.2	12.2	1992	11	BC002099		BC002099 Mus muscu
21	211.8	11.4	910	14	BQ681359		BQ681359 AGENCOURT
22	210.2	11.3	937	13	BI687408		BI687408 603315130
c	206.2	11.1	412	12	BF770342		BF770342 RC1-IT001
23	201	10.8	867	14	BQ888542		BQ888542 AGENCOURT
24	200.6	10.8	844	9	AJ446359		AJ446359 AJ446359
25	191.6	10.3	659	10	AW913297		AW913297 uf51d04.y
26	188.4	10.2	1051	9	AL544542		AL544542 AL544542
27	182.2	9.8	595	13	BI536809		BI536809 396201 MA
28	181.8	9.8	244	9	AA672571		AA672571 vo60e05.r
29	181.6	9.8	581	13	BI681932		BI681932 461444 MA
30	181.6	9.8	331	10	AW899099		AW899099 CM4-NM008
31	181	9.8	331	10	AW899099		AW899099 CM4-NM008
32	178.4	9.6	753	13	BI452907		BI452907 603170249
33	178.4	9.6	847	9	AJ445426		AJ445426 AJ445426
c	168.2	9.1	261	12	BF928435		BF928435 CM3-NT018
34	168.2	9.1	261	12	BF928435		BF928435 CM3-NT018
35	166.6	9.0	454	9	AI962024		AI962024 wt42a02.x
36	161	8.7	276	9	AA362346		AA362346 EST71776
37	160.6	8.7	644	10	AW975596		AW975596 EST387705
38	156.2	8.4	1059	14	BM919221		BM919221 AGENCOURT
39	156	8.4	1009	13	BM469621		BM469621 AGENCOURT
40	152.2	8.2	903	9	AL541451		AL541451 AL541451
c	150	8.1	416	9	AA713768		AA713768 NV82f02.s
41	150	8.1	488	10	BE626188		BE626188 ut83h11.x
42	149.8	8.1	494	10	BE178695		BE178695 PM4-HT060
43	149.8	8.1	494	10	BE178695		BE178695 PM4-HT060
c	148.6	8.0	497	10	BE690562		BE690562 uw55f09.x
44	148.6	8.0	497	10	BE690562		BE690562 uw55f09.x
45	147.8	8.0	924	9	AL550650		AL550650 AL550650

ALIGNMENTS

RESULT 1  
BC007679  
LOCUS  
DEFINITION  
Homo sapiens, Similar to purinergic receptor P2X, ligand-gated ion channel, 7, clone IMAGE:3628076, mRNA.  
ACCESSION  
BC007679  
VERSION  
BC007679.1  
KEYWORDS  
HGC.  
SOURCE  
Homo sapiens.  
ORGANISM  
Homo sapiens  
REFERENCE  
1 (bases 1 to 3013)  
AUTHORS  
Strausberg R.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (11-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
REMARK  
NIH-MGC Project URL: http://mgc.nci.nih.gov  
COMMENT  
Contact: MGC help desk  
Email: cgaabs@mail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;  
Web site: http://www.nisc.nih.gov/

BC007679 3013 bp mRNA linear HTC 12-JUL-2001  
Homo sapiens, Similar to purinergic receptor P2X, ligand-gated ion channel, 7, clone IMAGE:3628076, mRNA.

QY	5	CGCAGGAGGAGGCTGTCCACCATGCGCGCCCTGCTGCAGCTGCAGTGTGATGTTTTCAGTA	64
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QY	65	TGAGACGAACAAGATCACTCGGATCCAGACATGAATATGGCCACCAATTAAGTGGTCTTT	124
Db	89	TGAGACGAACAAGATCACTCGGATCCAGACATGAATATGGCCACCAATTAAGTGGTCTTT	148
QY	125	CCAGTGCATCACTTTTCTACGTTTGCCTTTGCTCTGGTGTAGTGACAGTGTACACGG	184
Db	149	CCAGTGCATCACTTTTCTACGTTTGCCTTTGCTCTGGTGTAGTGACAGTGTACACGG	200
QY	185	GAAGAGCCTGTCAATCAGTTCTGTGCACACCAAGGTGAAGGGATAGCAGAGGTGAAGA	244
Db	209	GAAGAGCCTGTCAATCAGTTCTGTGCACACCAAGGTGAAGGGATAGCAGAGGTGAAGA	268
QY	245	GGAGATCGGAGGATGAGTGAAGAAGTTGGTGTGCACAGTGTCTTTGACACCGCAGACTA	304
Db	269	GGAGATCGTGGAGATGAGTGAAGAAGTTGGTGTGCACAGTGTCTTTGACACCGCAGACTA	328
QY	305	CACCTCCCTTTGCAGGGGAACCTCTTCTTCGTGTATGACAAACTTCTCAAAAACAAGG	364
Db	329	CACCTCCCTTTGCAGGGGAACCTCTTCTTCGTGTATGACAAACTTCTCAAAAACAAGG	388
QY	365	CCAGACGACGGTGTGTCCCGAGTATCCACCCCGCAGGAGGTCTGTTCCTCTCAGCG	424
Db	389	CCAGACGACGGTGTGTCCCGAGTATCCACCCCGCAGGAGGTCTGTTCCTCTCAGCG	448
QY	425	AGTTGTAAAGAGGATGGATGGACCCCGCAGACCAAGGAATTCAGACCGGAAGGTGT	484
Db	449	AGTTGTAAAGAGGATGGATGGACCCCGCAGACCAAGGAATTCAGACCGGAAGGTGT	485
QY	485	AGTYATGAAGGGAACCGACAGACCTGTGAAGTCTCTGCTTGGTGCCCATCGAGGCACT	544
Db	486	-----	485
QY	545	GGAGAGCCCCCGCCTGCTCTTGAACAGTGCAGGAACTTCACCTGTGCTCATCAA	604
Db	486	-----GGCCTGTCTCTTGAACAGTGCAGGAACTTCACCTGTGCTCATCAA	531
QY	605	GAACAATATCGACTTCCCGGCGCAACTACACCCAGGAAACATCTTGCACAGTTTAA	664

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Db 1672 CCCTGGAGATCCCGAAAGAGTTTCGAAGAGTGAAGGAGTACAGTGGCTTCAAGAG 1731
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Db 1732 TCCTTACTGAAGCCAGGACCGTGGCTCAAGTCTGTATATCCACCGCTT 1780

RESULT 2
LOCUS B1861622
DEFINITION 603390486f1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5399565 5',
mRNA sequence.
ACCESSION B1861622
VERSION B1861622.1 GI:16002369
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 795)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaops-remail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12018 row: k column: 22
High quality sequence stop: 772.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:5399565"
/clone_lib="NIH_MGC_87"
/tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 176 a 231 c 228 g 160 t
ORIGIN

Query Match 36.4%; Score 675.2; DB 13; Length 795;
Best Local Similarity 97.7%; Pred. No. 3e-171;
Matches 707; Conservative 8; Mismatches 6; Indels 3; Gaps 3;

QY 1116 CGTCCCATATTTATCCCTGGTGCAGTGTCTGACCCGACATTAAGATATGTCTTTT 1235
Db 1 CGTCCCATATTTATCCCTGGTGCAGTGTCTGACCCGACATTTAAAGATATGTCTTTT 120
QY 1176 TACAGGAAGAGTGGAGTCCATTTGTGGAGCCCAAGCCGACATTAAGATATGTCTTTT 1235
Db 61 TACAGGAAGAGTGGAGTCCATTTGTGGAGCCCAAGCCGACATTTAAAGATATGTCTTTT 120
QY 1236 GTGGATGAATCCCATAGGATGTGTGAACACGACGCTACTAGGAGAGTCTGCAAGAT 1295
Db 121 GTGGATGAATCCCATAGGATGTGTGAACACGACGCTACTAGGAGAGTCTGCAAGAT 180
QY 1296 GTCAAGGGCCCAAGAGTCCCAAGACCTGTGATGGACTTCACAGATTTGTCCAGGCTGCC 1355
Db 181 GTCAAGGGCCCAAGAGTCCCAAGACCTGTGATGGACTTCACAGATTTGTCCAGGCTGCC 240

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QY 1356 CTGGCCCTCATGACACACACCCCGATTCTCTGGACAAACAGAGAGATACRGCTCTTAGA 1415
Db 241 CTGGCCCTCATGACACACACCCCGATTCTCTGGACAAACAGAGAGATACRGCTCTTAGA 300
QY 1416 AAGGAGGCGACTCTTAGATATCCAGGATAGCCCTGTCTGGTGCAGTGTGGAAAGTGCCTC 1475
Db 301 AAGGAGGCGACTCTTAGATATCA-GGATAGCCCGCTGTGGTGCAGTGTGGAAAGTGCCTC 359
QY 1476 CCATCTCAACTCCCTGAGAGCCACAGTGTCTGGAGGAGTGTCTGCTGCCGGAAGAGCGG 1535
Db 360 CCATCTCAACTCCCTGAGAGCCACAGTGTCTGGAGGAGTGTCTGCTGCCGGAAGAGCGG 419
QY 1536 GGGGCTGTGATCAACACCTCAGACTCTTCCAGAACTGTCTGCTCCAGACAGTCTCTG 1595
Db 420 GGGGCTGTGATCAACACCTCAGACTCTTCCAGAACTGTCTGCTCCAGACAGTCTCTG 479
QY 1596 CAGTTCCTCTCTCTACAGGAGCCCTTGTCTGCGCTGGATGTGGATTCACCAACAGC 1655
Db 480 CAGTTCCTCTCTCTACAGGAGCCCTTGTCTGCGCTGGATGTGGATTCACCAACAGC 539
QY 1656 CGGCTGGGCGACTGTGCTTACAGTGTACGCAACCTGCGCTCGGCTCCAGGAGCATG 1715
Db 540 CGGCTGGGCGACTGTGCTTACAGTGTACGCAACCTGCGCTCGGCTCCAGGAGCATG 599
QY 1716 GCTGAC-TTTGGCATCTGCGGCGAGTGTCTGCGCTGGAGTCCGGAAGAGTTTCCRAA 1774
Db 600 GCTGAC-TTTGGCATCTGCGGCGAGTGTCTGCGCTGGAGTCCGGAAGAGTTTCCRAA 659
QY 1775 GAGTGAAGGCGAGTACAGTGTCTCAAGAGTCC-TTACTGAAGCCAGGACCGCTGGTCA 1833
Db 660 GAGTGAAGGCGAGTACAGTGTCTCAAGAGTCC-TTACTGAAGCCAGGACCGCTGGTCA 719
QY 1834 CGTC 1837
Db 720 CGTC 723

RESULT 3
LOCUS BF347747
DEFINITION 602022588f1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4158189
5', mRNA sequence.
ACCESSION BF347747
VERSION BF347747.1 GI:11295342
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 946)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaops-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9433 row: o column: 22
High quality sequence stop: 706.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:4158189"
/clone_lib="NCI_CGAP_Brn67"
/tissue_type="anaplastic oligodendroglioma with lp/19q
loss"
/lab_host="DH10B (T1 phage-resistant)"

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size-selected for average insert size 2.3 kb and normalized to R01 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH\_MGC Library."

BASE COUNT 244 a 238 c 247 g 203 t  
ORIGIN

Query Match 34.8%; Score 645.4; DB 13; Length 932;  
Best Local Similarity 94.1%; Pred. No. 3.8e-163;  
Matches 712; Conservative 3; Mismatches 34; Indels 8; Gaps 4;

QY 421 ACCGAGTGTAAAGAGGATGGATGACCCGACAGCAAGAAATTCAGACCGAAGT 480  
|||||  
Db 469 ACCGAGTGTAAAGAGGATGGATGACCCGACAGCAAGAAATTCAGACCGAAGT 528  
|||||  
QY 481 GTGTAGTATYAGAGGAGCAAGCAAGACCTGTGAAGTCTCTGCTGTGCTGCCATCGAGG 540  
|||||  
Db 529 GTGTAGTATYAGAGGAGCAAGCAAGACCTGTGAAGTCTCTGCTGTGCTGCCATCGAGG 588  
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QY 541 CAGTGGAGAGCCCCCGCGCTCTCTCTTGAACAGTGGCGAAATTCACGTGCTCA 600  
|||||  
Db 589 CAGTGGAGAGCCCCCGCGCTCTCTCTTGAACAGTGGCGAAATTCACGTGCTCA 648  
|||||

QY 601 TCAAGAACAA-TATCGACTTCCCGGCCCAACTACACACGAG-AAACATCTCTCCAGG 658  
|||||  
Db 649 TCAAGAACAA-TATCGACTTCCCGGCCCAACTACACACGAG-AAACATCTCTCCAGG 708  
|||||

QY 659 TTTAAACATCACTGTACCTCCACAGACTCAGAAATCCACAGTGTCCCATTTCCG-AC 717  
|||||  
Db 709 TTTAAACATCACTGTACCTCCACAGACTCAGAAATCCACAGTGTCCCATTTCCG-AC 768  
|||||

QY 718 TAGGAGA-CATCTCCGAGAACAA-GGCGATAATTTTTCAGATGKGCATTCAGGGGG 775  
|||||  
Db 769 TAGGAGACCATCTTCGAGAACAAAGGGGGAATTAATTCAGAAATGTCCCACTTCAGGGGT 828  
|||||

QY 776 AATAATGGGCATTGGAGATCTACTGGGACTGCAACCTAGAACGTTGGTTCCATCACTGCC 835  
|||||  
Db 829 GAATATGGGCATTGAATTTACCTGGGACTGGCACTAGAACGTTGGTTCCATCACTGCC 888  
|||||

QY 836 TCCAAATACAGTTTCCTCGCTTGCCTTGACGACCAAGAC 871  
|||||  
Db 889 TCCAAATACAGTTTCCTCGCTTGCCTTGACGACCAAGACCAAGAC 924  
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RESULT 5  
BI603534  
LOCUS  
DEFINITION 60324436F1 NIH\_MGC\_96 Homo sapiens cDNA clone IMAGE:5286944 5', mRNA sequence.  
ACCESSION BI603534  
VERSION BI603534.1 GI:15496473  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 932)  
TITLE NIH-MGC http://mgc.nci.nih.gov/.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgyabs-r@mail.nih.gov  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM11725 row: g column: 09  
High quality sequence stop: 747.  
Location/Qualifiers  
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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5286944"  
/clone\_lib="NIH\_MGC\_96"  
/tissue\_type="hypothalamus"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag plusescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag plusescript KS+); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',

FEATURES  
SOURCE

RESULT 6  
BI603534  
LOCUS  
DEFINITION 602739207F1 NIH\_MGC\_49 Homo sapiens cDNA clone IMAGE:4869288 5', mRNA sequence.  
ACCESSION BI603534  
VERSION BI603534.1 GI:14077102

QY 5 CGCAGGAGGAGGCTGTCACTCGGCTCTGCTCCAGCTCCAGTGTATTTCCAGTA 64  
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Db 13 CGCAGGAGGAGGCTGTCACTCGGCTCTGCTCCAGCTCCAGTGTATTTCCAGTA 72  
|||||

QY 65 TGAGAGCAACAAAGTCACTCGGATCCAGAGCATGAATATGACCACTTAAGTGGTTCTT 124  
|||||  
Db 73 TGAGAGCAACAAAGTCACTCGGATCCAGAGCATGAATATGACCACTTAAGTGGTTCTT 132  
|||||

QY 125 CCACGTGATCATCTTTTCTACGTTTCTGCTCTGCTGTGAGTGACAAAGTGTACACGG 184  
|||||  
Db 133 CCACGTGATCATCTTTTCTACGTTTCTGCTCTGCTGTGAGTGACAAAGTGTACACGG 192  
|||||

QY 185 GAAAGAGCCCTGTCACTCTGTGACACCAAGTGTGAGGGGATGACAGAGTGAAGA 244  
|||||  
Db 193 GAAAGAGCCCTGTCACTCTGTGACACCAAGTGTGAGGGGATGACAGAGTGAAGA 252  
|||||

QY 245 GGAGATCGYGGAGAAATGAGTGAAGAAAGTTGGTGCACAGTGTCTTTGACACCGCAGACTA 304  
|||||  
Db 253 GGAGATCGYGGAGAAATGAGTGAAGAAAGTTGGTGCACAGTGTCTTTGACACCGCAGACTA 312  
|||||

QY 305 CACCTTCCCTTTGAGGGGAACTCTTTCTGCTGATGACAACTTTCTCAAAAACAGAGG 364  
|||||  
Db 313 CACCTTCCCTTTGAGGGGAACTCTTTCTGCTGATGACAACTTTCTCAAAAACAGAGG 372  
|||||

QY 365 CCAGAGACGCGGTGCTCCCGAGTATCCACCCGACGAGCGCTCTGCTCTCTGACCG 424  
|||||  
Db 373 CCAGAGACGCGGTGCTCCCGAGTATCCACCCGACGAGCGCTCTGCTCTCTGACCG 432  
|||||

QY 425 AGGTTGTAAAAAGGATGGATGGACCCGACAGCAAGAAATTCAGACCGGAGGTTGT 484  
|||||  
Db 433 AGGTTGTAAAAAGGATGGATGGACCCGACAGCAAGAAATTCAGACCGGAGGTTGT 492  
|||||

QY 485 AGTATGTAAGGGAACCAAGAGACCTGTGAAGTCTCTGCTGTGCTGCCATPCGAGGAGT 544  
|||||  
Db 493 AGTATGTAAGGGAACCAAGAGACCTGTGAAGTCTCTGCTGTGCTGCCATPCGAGGAGT 552  
|||||

QY 545 GGAAGAGGCCCCCGCGCTGCT-CTCTTGAACAGTGGCGGAAA--CTTCACTGTGCTCAT 601  
|||||  
Db 553 GGAAGAGGCCCCCGCGCTGCTCTCTTGAACAGTGGCGGAAA--CTTCACTGTGCTCAT 612  
|||||

QY 602 CAAGAAACAATATCGACTTCCCGGCCCAACTACACCGAGAAACATCT--GCCAGGT 659  
|||||  
Db 613 CAAGAAACAATATCGACTTCCCGGCCCAACTACACCGAGAAACATCT--GCCAGGT 672  
|||||

QY 660 TTAACATCACTTGTACCTTCCACAGACTCAAGATPCACACA---GTGCCATTTCCGA 716  
|||||  
Db 673 TTAACATCACTTGTACCTTCCACAGACTCAAGATPCACACA---GTGCCATTTCCGA 732  
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QY 717 CTAGGAGACATCTCCGAGAACAGGGGATAATTTT 753  
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Db 733 TAAGGAGACATCTCCCGAGAAACAGGGGAGTACTT 769  
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[illegible]



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QY 714 CGACTAGGACATCTTCGGAACACAGGCGATATTT 752
Db 769 CGACTAGGACCATCTACGAGAAAACGGCGATCAT 807

RESULT 9
BF689446 908 bp mRNA linear EST 22-DEC-2000
LOCUS 602186810F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298811 5',
DEFINITION mRNA sequence.
ACCESSION BF689446
VERSION BF689446.1 GI:11974854
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 908)
JOURNAL NIH-MGC http://mgi.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM1155 row: c column: 04
High quality sequence stop: 668.

FEATURES
source
Location/Qualifiers
1..908
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/clone="IMAGE:4298811"
/clone_lib="NIH_MGC_49"
/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GACACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library. |"
BASE COUNT 237 a 208 c 260 g 203 t
ORIGIN
Query Match 29.58; Score 547.4; DB 12; Length 908;
Best Local Similarity 92.94; Pred. No. 1.2e-136;
Matches 659; Conservative 3; Mismatches 34; Indels 13; Gaps 8;

QY 5 CGCAGGAGGAGGCTGCACCATGCCGCTGCTGCAGTGCAGTGTATTTCCAGTA 64
Db 49 CGCAGGAGGAGGCTGCACCATGCCGCTGCTGCAGTGCAGTGTATTTCCAGTA 108

QY 65 TGAGACGACAAAGTCACTCGGATCCAGACATGAATATGGACCATTAAGTGTCTT 124
Db 109 TGAGACGACAAAGTCACTCGGATCCAGACATGAATATGGACCATTAAGTGTCTT 168

QY 125 CCACGTGATCATCTTTCTACCTTTGCTTCTGCTGAGTGACAACTGTCCACGG 184
Db 169 CCACGTGATCATCTTTCTACCTTTGCTTCTGCTGAGTGACAACTGTCCACGG 227

QY 185 GAAAGAGCCTGTCATCATGTTCTGTGCACACCAAGTGAAGGGATAGACAGAGTGAAGA 244
Db 228 GAAAGAGCCTGTCATCATGTTCTGTGCACACCAAGTGAAGGGATAGACAGAGTGAAGA 287

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(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

BASE COUNT	214 a	199 c	216 g	188 t	
ORIGIN					
Query Match	26.9%;				Score 498.6; DB 10;
Best Local Similarity	81.7%;				Pred. No. 1.7e-123;
Matches	677;				Conservative 3; Mismatches 47; Indels 102; Gaps 5
QY	10	GGAGGGAGGCTGCACCATGCGCGGCTGCTGCAGCTGCAGTGAATGTTTCCAGTATGAGA	69		
DB	5	GGAGGGAGGCTGCACCATGCGCGGCTGCTGCAGTGCAGTGAATGTTTCCAGTATGAGA	64		
QY	70	CGAACAAAGTCACCTCGGATCCAGACCAATGAATATGGCACCAATTAAGTGGTTCCTCCAG	129		
DB	65	CGAACAAAGTCACCTCGGATCCAGACCAATGAATATGGCACCAATTAAGTGGTTCCTCCAG	124		
QY	130	TGATCATCTTTTCTACTAGTTTCTTCTGTGTGTAGTGCACAGCTGTACACGGGAAAG	189		
DB	125	TGATCATCTTTTCTACTAGTTTCTTGTGTGTAGTGCACAGCTGTACACGGGAAAG	18		
QY	190	AGCCTGTCTATCAGTTCTGTSCACACCAAGGTGAAGGGGATAGCAGAGTGAAGAGGAGA	249		
DB	184	AGCCTGTCTATCAGTTCTGTSCACACCAAGGTGAAGGGGATAGCAGAGTGAAGAGGAGA	243		
QY	250	TCGTGGAGAATGAGTGAAGAGTTGGTGACAGTGTCTTT-TGACACCGCAGACTACAC	308		
DB	244	TCGTGGAGAATGAGTGAAGAGTTGGTGACAGTGTCTTTGTGACACCGCAGACTACAC	303		
QY	309	TTCCTTTTGACGGGGAACTCTTTCTGTGTGTAGTGCACAACTTCTCAAAACAGAGGCCAA	368		
DB	304	TTCCTTTTGACGGGGAACTCTTTCTGTGTGTAGTGCACAACTTCTCAAAACAGAGGCCAA	363		
QY	369	GAGCAGCGGTTGTGTCCGAGTATCCACCGG--CAGGACGCTCTGTTCCTCTGACCGAG	426		
DB	364	GAGCAGCGGTTGTGTCCGAGTATCCACCGGTCAGTACGCTCTGTTCCTCTGACCGAG	423		
QY	427	GTTGTAAAGAGGATGGTGGACCGCAGACGACAAAGGAATTCAGACCGGAAGTGTGTAG	486		
DB	424	GTTGTAAAGAGGATGGTGGACCGCAGACGACAAAGGAATTCAGACCGGAAGTGTGTAG	486		
QY	487	TYATGAGGAGAACAGAGAGACTCTGTGAGTCTCTGCCTGGTGGCCCATCGAGCGACTGG	546		
DB	459	-----	458		
QY	547	AAGAGGCCCCCGGCGCTGCTCTTTGAACAGTGCAGAACTTCACTGTGCTCATCAAGA	606		
DB	459	-----GGCCTGCTCTTTGAACAGTGCAGAACTTCACTGTGCTCATCAAGA	506		
QY	607	ACATATGCACTTCCCGGCCACAACTACACACGAGAAACATCTGCGAGGTTTAAACA	666		
DB	507	ACATATGCACTTCCCGGCCACAACTACACACGAGAAACATCTGCGAGGTTTAAACA	566		
QY	667	TCACCTGTACTTCCACAGACTCAGATCCACAGTGTCCCATTTTCGAGCTAGGAGACA	726		
DB	567	TCACCTGTGTACTTCCACAGACTCAGATCCACAGTGTCCCATTTTCGAGCTAGGAGACA	626		
QY	727	TCTTCCGAGAAACAGCGGATTAATTTTTCAGATGKGCATTCAGGGCGGAATATGSGCA	786		
DB	627	TCTTCCGAGAAACAGCGGATTAATTTCCGATGTGGGCAATTCAGCGCGGATTAATGGCA	686		
QY	787	TTGAGATCTACTGGGATCGAACCTTAGACGGTTGGTTCATCATCTGTC	835		
DB	687	-TGAGATCTACTGGGATCGAACCTTAGACGGGTCCTCATGCGGCA	734		
RESULT 11					
BF690388/c					
LOCUS	1022 bp				mRNA linear
DEFINITION	60218681071 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298811				EST 22-DEC-2000
ACCESSION	BF690388				mRNA sequence.
VERSION	BF690388.1				GI:11975796

KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 1022)
TITLE	NIH-MGC <a href="http://mgc.ncbi.nlm.nih.gov/">http://mgc.ncbi.nlm.nih.gov/</a> .
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cyapbs-remail.nih.gov Tissue Procurement: ATCC/DCTD/DFP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: L1CM155 row: c column: 04 High quality sequence start: 11 High quality sequence stop: 688. Location/Qualifiers 1..1022 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4298811" /clone_lib="NIH_MGC_49" /tissue_type="melanotic melanoma, high MDR (cell line)" /lab_host="DH10B (phage-resistant)" /note="organ: skin; Vector: pOTB7; site:1: XhoI; site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library.!"
BASE COUNT	223 a 283 c 294 g 222 t
ORIGIN	
Query Match	26.3%; Score 487.6; DB 12; Length 1022;
Best Local Similarity	95.0%; Pred. No. 1.8e-120;
Matches 496; Conservative	6; Mismatches 20; Indels 0; Gaps 0;
QY	1332 TTCCAGAGATTTCACAGCGTCGCCCTCGACGACACACCCCGGATTCCTGGACAA 1391
Db	715 TTCCAGAGCCTTGTCCAGCGTCCCTGGCCCTTCATGACACACCCCTCGATTTCTGGACAA 656
QY	1392 CCAGAGGAGATACRGCTGCTTTAGAAAGAGGCGGACTCCTAGATCCAGGATAGCCCGTC 1451
Db	655 CCAGAGGAGATACAGCTGCTTAGAAGAGGAGCGACTCCTAGATCCAGGAGATAGCCCGTC 596
QY	1452 TGGTGCCAGTGTGGAAGCTGCCTCCCATCTCAACTCCCTGAGRGCCACAGGTGCCTGGAG 1511
Db	595 TGGTGCCAGTGTGGAAGCTGCCTCCCATCTCAACTCCCTGAGAGGCCACAGGTGCCTGGAG 536
QY	1512 GMGCTGTGCTGCCGAAAGACGGGGGGCTGCATCACCACTCAGAGCTGTTCAGGAAG 1571
Db	535 GAGCTGTGCTGCCGAAAGACGGGGGGCTGCATCACCACTCAGAGCTGTTCAGGAAG 476
QY	1572 CTGCTCCTCTCCAGACAGCTCTCGAGTTTCCTGCTGTCTACCAAGAGCCCTTGTGCGG 1631
Db	475 CTGCTCCTCTCCAGACAGCTCTCGAGTTTCCTGCTGTCTACCAAGAGCCCTTGTGCGG 416
QY	1632 CTGAGTGTGGAATTCACACACCGCGCTGCGGCACGTGTGCTCTACAGGTGTCTAGCCACC 1691
Db	415 CTGGAATGTGGATTCACCAACACGCGGCTGCGGCACGTGTGCTCTACAGGTGTCTAGCCACC 356
QY	1692 TGGCGCTTCGGCTCCAGGACATGGCTGACTTTGCCATCTGCCAGCTGCTGCCGCTGG 1751
Db	355 TGGCGCTTCGGCTCCAGGACATGGCTGACTTTGCCATCTGCCAGCTGCTGCCGCTGG 296

Db	288	GGAGATCGTGGAGAAATGAGTGAAGAGTGGTGCACAGTGC-TTGACACCGCAGACTA	346
QY	305	CACCTTCCTTTCGACAGGGAACCTCTTCTTCGTGATGACAACTTCTCAAAACAGAAGG	364
Db	347	CACCTTCCC-TTGACAGGGAACCTCTTCTTCGTGATGACAACTTCTCAAAACAGAAGG	405
QY	365	CCAAGAGCAGCGGTTGTGTCGCGAGTATCCACCGCAGGACGCTGTGTCTCTGACCG	424
Db	406	CCAAGAGCAGCGGTTGTGTCGCGAGTATCCACCGCAGGACGCTGTGTCTCTGACCG	465
QY	425	AGTTGTAAGGAGGATGATGATGACCGCAGAGCAAGGAATTCAGAC	472
Db	466	AGTTGTAAGGAGGATGATGATGACCGCAGAGCAAGGAATTCAGAC	513
<p>RESULT 13</p> <p>BO554327 H4027E01-5 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone</p> <p>LOCUS H4027E01 5', mRNA sequence.</p> <p>ACCESSION BO554327</p> <p>VERSION 1</p> <p>KEYWORDS GI:21455215</p> <p>SOURCE house mouse.</p> <p>ORGANISM Mus musculus</p> <p>REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.</p> <p>AUTHORS 1 (bases 1 to 642)</p> <p>VanBuren,V., Piao,Y., Dudekula,D.B., Qian,Y., Carter,M.G., Martin,P.R., Stadg,C.A., Bassey,J., Alba,K., Hamatani,T., Kargul,G.J., Luo,A.G. and Ko,M.S.H.</p> <p>TITLE Assembly, verification, and initial annotation of NIA 7.4K mouse cDNA clone set</p> <p>JOURNAL Unpublished (2002)</p> <p>COMMENT Other_ESTS: H4027E01-3</p> <p>Contact: Yong Qian</p> <p>Laboratory of Genetics</p> <p>National Institute on Aging/National Institutes of Health</p> <p>333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA</p> <p>Email: cdna@igsun.grc.nia.nih.gov</p> <p>This clone set has been freely distributed to the community. Please visit <a href="http://igsun.grc.nia.nih.gov/cDNA/NIA_7.4k.html">http://igsun.grc.nia.nih.gov/cDNA/NIA_7.4k.html</a> for details.</p> <p>Plate: H4027 row: E column: 01</p> <p>Seq primer: -21M13 Reverse</p> <p>High quality sequence stop: 642</p> <p>POLYA=No.</p> <p>FEATURES</p> <p>Location/Qualifiers</p> <p>1..642</p> <p>/organism="Mus musculus"</p> <p>/strain="C57BL/6"</p> <p>/db_xref="niaEST:H4027E01-5"</p> <p>/db_xref="taxon:10090"</p> <p>/clone="H4027E01"</p> <p>/clone_lib="NIA Mouse 7.4K cDNA Clone Set"</p> <p>/sex="mixed"</p> <p>/dev_stage="mixed"</p> <p>/lab_host="DH10B"</p> <p>/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This clone is among a rearrayed set of 7,407 clones from more than 20 cDNA libraries."</p> <p>BASE COUNT 133 a 199 c 179 g 131 t</p> <p>ORIGIN</p> <p>Query Match 21.6%; Score 400.8; DB 14; Length 642;</p> <p>Best Local Similarity 80.2%; Pred. No. 4.1e-97;</p> <p>Matches 465; Conservative 4; Mismatches 111; Indels 0; Gaps 0;</p>			
QY	1242	GAATCCACATTAGATGGTGAACACACACCTACTACGAGCAAGTCTGCAGATGTCAG	1301
Db	1	GAGCGCACAATTGGATGGTGGACGACGCTGTGGGAAAGCTGCAAGTGTGAAA	60
QY	1302	GGCCACGAAGTCCGAAGACCTGATGGACTTCACAGATTTGTCCAGCTGTGCGCTGGCC	1361



Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov  
Plate: L1A9429 row: g column: 13  
High quality sequence start: 39  
High quality sequence stop: 541.

## FEATURES

## SOURCE

1..555  
/Location/Qualifiers  
loss"  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4156452"  
/clone\_lib="NCI\_CGAP\_Brn67"  
/tissue\_type="anaplastic oligodendroglioma with lp/19q loss"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: Brain; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI\_CGAP Library."

BASE COUNT 144 a 134 c 154 g 123 t  
ORIGIN

Query Match 20.18; Score 373; DB 12; Length 555;  
Best Local Similarity 95.8%; Pred. NO. 1.2e-89;  
Matches 457; Conservative 1; Mismatches 11; Indels 8; Gaps 7;  
QY 6 GCAGGAGGAGGCTGCACCATGCCGCCCTGTCGACGTCGACGTCGACGTCGACGTCAT 65  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
52 GCAGGAGGAGGCTGCACCATGCCGCCCTGTCGACGTCGACGTCGACGTCGACGTCAT 110  
QY 66 GAGACGAACAAAGTCTCGGATCCAGAGCATGAATTATGGCACCATTAAAGTGGTTCTTC 125  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
111 GAGACGAACAAAGTCTCGGATCCAGAGCATGAATTATGGCACCATTAAAGTGGTTCTTC 170  
QY 126 CACGTGATCATCTTTTCCTAC-- GTTTCCTTGTCTGTGTGAGTGAACAAGCTGT-ACCAG 182  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
171 CACGTGATCATCTTTTCCTAC-- GTTTCCTTGTCTGTGTGAGTGAACAAGCTGT-ACCAG 230  
QY 183 CGGAAGAGCTGTATCATCTGTGTGCACACCAAGCTGAAGGGGATACGAGAGTGAAA 242  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
231 CGGAAGAGCTGTATCATCTGTGTGCACACCAAGCTGAAGGGGATACGAGAGTGAAA 290  
QY 243 GAGGAGATCGYVGA-GAATGGAGTGAAGAAGTGTGTGCACAGTGTCTTTTGACACCGCAGA 301  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
291 GAGGAGATCGTGGACGAATGGAGTGAAGAAGTGTGTGCACAGGCTCTTTGACACCGCAGA 350  
QY 302 CTACACCTTCCTTTTCAGGGGACTCTTCTTCTGTGNTGACAAACTTTCACAAACAGA 361  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
351 CTACACCTTCCTTTTCAGGGGAACTCTTCTTCTGTGATGACAAACTTTCACAAACAGA 410  
QY 362 AGGCCAAGACGAGCGGTGTGTCGCCAGTATCCACCGCAGGACGCTCTGTTCCTCTGA 421  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
411 AGGCCAAGACGAGCGGTGTGTCGCCAGTATCCCA-CCGACGACGCTCTGTTCCTCTGA 469  
QY 422 CCGAGGTGTGA-AAAGGATGATGG-ACCGCAGACGCAAAAGAAATTCAGACCGGA 476  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
470 CCGAGGTGTGAACAGAGGATGGCTGGCACCACCGCAGACGCAAAAGAAATTCAGACCGGA 526

Search completed: July 18, 2003, 19:00:05  
Job time : 2721 secs